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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 3, 2003, 13:38:24 ; Search time 1844.31 Seconds
(without alignments)
11219.411 Million cell updates/sec

Title: US-09-576-424-9
Perfect score: 711
Sequence: 1 atgggggtcccgctcagct.....ccctacagaatgttcacga 711

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
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- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
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- 20: em_om.*
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- 22: em_ov.*
- 23: em_pat.*
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- 27: em_sts.*
- 28: em_un.*
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- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	711	100.0	711	6	ARI08866	ARI08866 Sequence
2	582.6	81.9	935	6	ARI135362	ARI135362 Sequence
3	575.4	80.9	790	9	AB064208	AB064208 Homo sapi
4	573	80.6	870	9	HSIGLV	X14583 Human mRNA
5	571.2	80.3	903	9	BC020233	BC020233 Homo sapi
6	570.6	80.3	827	9	AB064143	AB064143 Homo sapi
7	566.6	79.7	800	9	AB064188	AB064188 Homo sapi
8	566.4	79.7	919	9	BC022098	BC022098 Homo sapi
9	566	79.6	815	9	AB064149	AB064149 Homo sapi
10	562.8	79.2	812	9	AB064148	AB064148 Homo sapi
11	562.8	79.2	816	9	AB064147	AB064147 Homo sapi
12	562.4	79.1	827	9	AB064219	AB064219 Homo sapi
13	562.2	79.1	750	9	HSIGVL027	X57817 Human rearr
14	560	78.8	747	9	HSIGVL006	X57806 Human rearr
15	558	78.5	821	9	AB064141	AB064141 Homo sapi
16	558	78.5	824	9	AB064227	AB064227 Homo sapi
17	557.6	78.4	804	9	AB064172	AB064172 Homo sapi
18	556.4	78.3	790	9	AB064206	AB064206 Homo sapi
19	556.4	78.3	824	9	AB064226	AB064226 Homo sapi
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21	554.8	78.0	816	9	AB064150	AB064150 Homo sapi
22	554.4	78.0	790	9	AB064169	AB064169 Homo sapi
23	554.4	78.0	803	9	AB064166	AB064166 Homo sapi
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25	552.8	77.7	788	9	AB064171	AB064171 Homo sapi
26	552.8	77.7	789	9	AB064170	AB064170 Homo sapi
27	552.8	77.7	819	9	AB064151	AB064151 Homo sapi
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32	547.8	77.0	802	9	HSIGVL032	X57822 Human rearr
33	546.2	76.8	810	9	HSIGVL025	X57815 Human rearr
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35	545.6	76.7	9472	6	AX287808	AX287808 Sequence
36	545	76.7	789	9	AB064205	AB064205 Homo sapi
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ALIGNMENTS

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LOCUS	ARI08866	Sequence 9	from patent US 6113898.			
DEFINITION	ARI08866					
ACCESSION	ARI08866					
VERSION	ARI08866.1	GI:12825142				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 711)					
AUTHORS	Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.					
TITLE	Human B7.1-specific primatized antibodies and transfectomas					
JOURNAL	expressing said antibodies					
	Patent: US 6113898-A 9 05-SEP-2000;					

FEATURES Location/Qualifiers
source i. 711
BASE COUNT 160 a 226 c 193 g 132 t
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Query Match 100.0%; Score 711; DB 6; Length 711;
Best Local Similarity 100.0%; Pred. No. 4.9e-174;
Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCTGCTGCTCTGGCTCCAGGTGCACGATCT 60
DB 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCTGCTGCTCTGGCTCCAGGTGCACGATCT 60
QY 61 GAGTCTGTCTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACCATC 120
DB 61 GAGTCTGTCTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACCATC 120
QY 121 TGTGCACTGGGAGCACTTCCAACTATGGAGGTATGATCTACATTGGTACCAGCAGCTC 180
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DB 661 CATGAAGGAGCAGCTGAGAGAGCAGTGGCCCTTACAGATGTTTCATGA 711

RESULT 2
AR135362
LOCUS
DEFINITION Sequence 20 from patent US 6135941.
ACCESSION AR135362
VERSION AR135362.1 GI:14476034
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 935)
AUTHORS Hillman,J.L., Lal,P., Tang,Y.Tom., Yue,H., Au-Young,J., Corley,N.C., Guegler,K.J. and Baughn,M.R.
TITLE Human immune system associated molecules

JOURNAL Patent: US 6135941-A 20 24-OCT-2000;
FEATURES Location/Qualifiers
source i. 935
BASE COUNT 216 a 299 c 248 g 172 t
ORIGIN
Query Match 81.9%; Score 582.6; DB 6; Length 935;
Best Local Similarity 89.8%; Pred. No. 1.1e-140;
Matches 637; Conservative 0; Mismatches 69; Indels 3; Gaps 1;
QY 4 AGGGTCCCGCTCAGCTCCTGGGGCTCTGCTGCTCTGGCTCCAGGTGCACGATCTGAG 63
DB 74 ATGGGCTGGTCT 133
QY 64 TCTGTCTTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACCATCTCG 123
DB 134 TCTGTCTTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACCATCTCC 193
QY 124 TGCACCTGGGAGCACCTCCAACTTGG---AGGTTATGATCTATGATTTGGTACCAGCAGCTC 180
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QY 181 CCAGGAACGGCCCCAACTCCTCATCTATGACATTAACAAGCGCCCTCAGGAATTTCT 240
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DB 554 AGTGACTTCTACCGGAGCGGTGACAGTGGCTTGAAGGAGATAGAGCCCGCTCAAG 613
QY 541 GCGGAGTGGAGACCAACACCTCCAAACAAAGCAACAAGTACCGGCGCAGCAGC 600
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DB 734 CATGAAGGAGCAGCTGAGAGAGCAGTGGCCCTTACAGATGTTTCAT 782

RESULT 3
AB064208
LOCUS
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:L68.
ACCESSION AB064208
VERSION AB064208.1 GI:21669622
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 935)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE

AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirose, Y., Kakita, M., Suzuki, K., Torii, H., Ueki, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.

TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 790)

AUTHORS Kurosawa, Y.

TITLE Direct Submission

JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;

Kutsukake-cho, Toyosake 470-1192, Japan

(E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)

Please visit our web site

URL: <http://www.fujita-hu.ac.jp/immunity/>.

FEATURES

source

1..790

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/clone="L68"

/note="mixture of tissues: tonsils, umbilical cords,

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Qy 479 TAAGTGACTTCTACCGGAGCCGTGACAGTGGCTTGAAGCGAGATAGCAGCCCGTCA 538

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RESULT 4

HSIGLV

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

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BASE COUNT

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Matches 624; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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QY 601 TACCTGAGCTGACGCTCAGCAGTGAAGTCCACAGAGCTACAGCTGCCAGGTCAAG 660
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RESULT 5
BC020233
LOCUS      903 bp mRNA linear PRI 03-JAN-2002
DEFINITION Homo sapiens, clone MGC:31936 IMAGE:4765518, mRNA, complete cds.
ACCESSION BC020233
VERSION BC020233.1 GI:18044240
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 903)
REFERENCE Strausberg,R.
            Direct Submission
            Submitted (19-DEC-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 40 Row: h Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomScan gene prediction, Similarity but not identity
to protein.

FEATURES

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Miura, K. and Kurosawa, Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
Unpublished
2 (bases 1 to 800)
Kurosawa, Y.
Direct Submission
Submitted (25-JUN-2001) Yoshihazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)
Please visit our web site
URL: http://www.fujita-hu.ac.jp/immunity/
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 919)
Direct Submission
Strausberg, R.
Submitted (24-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeeedi, Jacqueline
Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IPAL plate: 40 Row: n Column: 11
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DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:l8.
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VERSION AB064148.1 GI:21669502
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REFERENCE 1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 812)
AUTHORS Kurosawa, Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
(E-mail:kurosawafujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT Please visit our web site.
URL:http://www.fujita-hu.ac.jp/immunity/
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REFERENCE 1 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 816)

AUTHORS Kurosawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
 (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
 COMMENT Please visit our web site
 URL:http://www.fujita-hu.ac.jp/immunity/
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 REFERENCE
 AUTHORS
 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
 TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 827)
 AUTHORS Kurosawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
 (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
 COMMENT Please visit our web site
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X57817.1 GI:33733
Ig lambda light chain; immunoglobulin.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Direct Submission
Submitted (31-JAN-1991) H.G. Kloebeck, Inst fuer Physiologische
Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
2 (bases 338 to 384)
Combratio,G. and Kloebeck,H.G.
V lambda and J lambda-C lambda gene segments of the human
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Eur. J. Immunol. 21 (6), 1513-1522 (1991)
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VERSION Ig lambda light chain; immunoglobulin.
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Klobbeck,H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) H.G. Klobbeck, Inst fuer Physiologische
Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE
AUTHORS Combratio,G. and Klobbeck,H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur J Immunol. 21 (6), 1513-1522 (1991).
MEDLINE 91257162
PUBMED 1904362
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.
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DEFINITION region, partial cds, clone:11.
ACCESSION AB064141
VERSION AB064141.1 GI:21669488
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:15:24 ; Search time 969.606 Seconds
(without alignments)
11875.950 Million cell updates/sec

Title: us-09-576-424-9

Perfect score: 711

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Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq-length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: em_estpl:*

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16: em_estom:*

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18: em_gss_hum:*

19: em_gss_inv:*

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2	562.6	79.1	913	14	BQ708635
3	559	78.6	894	14	BQ708570
4	558.6	78.6	819	12	BQ708564
5	557.8	78.5	873	14	BQ712653
6	555.6	78.1	755	12	BQ755185

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9	551.6	77.6	910	12	BQ757147	602710516
10	549.4	77.3	857	14	BQ890529	AGENCOURT
11	549	77.2	764	12	BQ755548	602716230
12	546	76.8	817	13	BI835917	603085650
13	545.4	76.7	896	12	BQ688967	602388530
14	544.8	76.6	823	12	BQ688957	602850951
15	544.6	76.6	849	12	BQ756887	602710380
16	544.6	76.6	1124	14	BM918688	AGENCOURT
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ALIGNMENTS

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BQ711292

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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AGENCOURT_8353826 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6278335
5', mRNA sequence.

BQ711292 1 GI:21850191

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgs.nci.nih.gov/>

1 (bases 1 to 956)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: AGencourt Bioscience Corporation

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence start: 10

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Location/Qualifiers

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laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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(EcoRV site is destroyed upon cloning). Average insert
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tracking code 025. Note: this is a NIH MGC Library."
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EST.
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1060)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12364 row: g column: 04
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of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned.
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
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Qy 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGCGAGAGGTTCACCATC 120
Db |||||
Qy 109 CAGTCTGTGTTGACGACGCGCCCTCAGTGTCTGCGGGCCCCAGGAGGTTCAAGTCT 168
Db |||||
Qy 121 TCGTGACTGGGAGCAGCTTCCAAATTTGGAGGTATGATCTACATTTGGTACCGAGCAGTCT 180
Db |||||
Qy 169 TCCTGTCTCTGGAAGCAGTGTGCAACATTTGGAGTAATTTAGTTTCTCTGGTACCAACACCTC 228
Db |||||
Qy 181 CCAGGAACGGCCCCCAACTCTCTCTATGATTAACAGGACCCCTCAGGAATTTCT 240
Db |||||
Qy 229 CCAGGGGACGCCCCCATACTCTCTCTCAATTTATGACAATAAAGCGACCCCTCAGGAATTC 288
Db |||||

159	TCTGTCTCTGGAAGCAGCTCCAA	218	CTTGGGAATAATTATGTCTCTGGTACAGCAGCTC	218
181	CCAGGAACGGCCCCCAAACTCCTCTCATCTATGACATTAACAAGCGACCCCTCAGGAATTTCT	240		240
219	CCAGGTACAGCCCCCGAACTCCTCATCTATGAAAATAGTAAGCGACCCCTCAGGGAATCTT	278		278
241	GACCGATTCTCTGGCTCAAAGTCTGGTACCGGGGCTCCCTGGGCCATCATCTGGGCTCCAG	300		300
279	GACCGATTCTCTGGCTCAAAGTCTGGGACGTCAGCGGCCCTGGCCCATCACCGGACTCCAG	338		338
301	ACTGAGGATGAGGCTGATTATTACTGCCAGTCCCTATGACAGCAGCGCTGAATGCTCAGGTA	360		360
339	ACTGGGACGAGGCGCGATTATTACTGCGGAA	398	CATGGGATGACAGCGCTCGTGGTGTGGGTG	398
361	TTCCGAGGAGGAGCCCGGCTGACCGCTCTAGCTCAGCGCAAGGCTGCCCTCGGTCACT	420		420
399	TTCCGCGGAGGGA	458	CCAACTGACCGTCTGAGTCAGCCCAAGGCTGCCCTCGGTCACT	458
421	CTGTTCCGCGCCTCCTCTGAGGAGCTTCAAGCCAA	480	CAGGCCACACTGGTGTGCTCATATA	480
459	CTGTTCCGCGCCTCCTCTGAGGAGCTTCAAGCCAA	518	CAGGCCACACTGGTGTGCTCATATA	518
481	AGTGACTTCTACCGGGAGCCGTGACAGTGGCTGGAAAGGCGGATAGCAGCCCCGTCAAG	540		540
519	AGTGACTTCTACCGGGAGCCGTGACAGTGGCTGGAAAGGCGGATAGCAGCCCCGTCAAG	578		578
541	GCGGGAGTGGAGACACACACACCTTCCAAA	600	CAAGCAACAACTAGTCGCGCCACGACGC	600
579	GCGGGAGTGGAGACACACACACCTTCCAAA	638	CAAGCAACAACTAGTCGCGCCACGACGC	638
601	TACCTGAGCCTGAGCGCTTGAGCAGTGGAAAGTCCCA	660	CAGAAGCTACAGCTGCCAGGTCCAGC	660
639	TACCTGAGCCTGAGCGCTTGAGCAGTGGAAAGTCCCA	698	CAGAAGCTACAGCTGCCAGGTCCAGC	698
661	CATGAGGAGGACACCGTGGAGAGACAGTGGCCCCCTACAGAAATGTTTCAAT	709		709
699	CATGAGGAGGACACCGTGGAGAGACAGTGGCCCCCTACAGAAATGTTTCAAT	747		747

RESULT 12					
BI835917					
LOCUS	BI835917	817 bp	mRNA	linear	EST 04-OCT-2001
DEFINITION	603085650F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5224645 5', mRNA sequence.				

FEATURES
SOURCE

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
-------	------------	-----------	---------	----------

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:14:13 ; Search time 158.886 Seconds
(without alignments)
10077.457 Million cell updates/sec

Title: US-09-576-424-9
Perfect score: 711
Sequence: 1 atgagggtcccgctcagct.....ccctacagaatgttcata 711

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21 - /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22 - /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23 - /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24 - /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	711	19	AAV35488
2	711	100.0	711	24	AA517246
3	709.4	99.8	711	18	AA672512
4	582.6	81.9	935	22	AAC66525
5	571.4	80.4	884	11	AAQ03609
6	565.2	79.5	762	22	AAC84209
7	558.8	78.6	5679	22	AAC84207
8	552.6	77.7	768	20	AA06953
9	552.6	77.7	768	20	AA06954

10	547	76.9	654	14	AAQ49835	Anti-HIV-1 recombi
11	546.2	76.8	810	23	AA587270	DNA encoding novel
12	540.2	76.0	705	18	AA62509	Primate anti-hu
13	540.2	76.0	705	19	AAV35484	Macaque primatized
14	540.2	76.0	705	24	AA517242	DNA sequence of a
15	533.2	75.0	651	19	AAV11293	Antibody HB4C5 lig
16	533.2	75.0	708	22	AAH47902	Human type antihum
17	532.2	74.9	915	24	ABN97248	Gene #3746 used to
18	532.2	74.9	915	24	ABK64815	Human benign prost
19	532.2	74.9	915	24	ABL65478	Lung cancer relate
20	530.2	74.6	895	22	AA666530	Human immune syste
21	523.6	73.6	708	22	AAH47904	Human type antihum
22	522.8	73.5	1845	22	ABL49526	Plasmid scFv(CC046
23	518.8	73.0	708	22	AAH47898	Human type antihum
24	510.6	71.8	891	22	AAC66528	Human immune syste
25	509.2	71.6	763	23	AA583480	DNA encoding novel
26	502.6	70.7	902	14	AAQ35100	Antibody D lambda
27	499.4	70.2	889	23	AA577073	DNA encoding novel
28	498.6	70.1	906	22	AAK51914	Human polynucleoti
29	496.4	69.8	951	23	AA590539	DNA encoding novel
30	494.4	69.5	783	23	AA583483	DNA encoding novel
31	494.4	69.5	876	23	AA583478	DNA encoding novel
32	493.8	69.5	888	21	AA95786	Human immune syste
33	487.4	68.6	1636	23	ABV22585	Human prostate exp
34	487.4	68.6	1636	23	ABV28405	Human prostate exp
35	486.6	68.4	756	23	AA583477	DNA encoding novel
36	484.2	68.1	885	19	AAV34321	Human secreted pro
37	482.6	67.9	879	19	AAV34304	Human secreted pro
38	480.6	67.6	1636	23	ABV22585	Human prostate exp
39	480.6	67.6	1636	23	ABV28405	Human prostate exp
40	477	67.1	926	20	AAZ24427	Human bladder tumo
41	475.2	66.8	807	23	AA583484	DNA encoding novel
42	470.4	66.2	872	9	AAH81655	VDJC regions of hu
43	468.4	65.9	702	18	AA62867	Ant-CD4 monkey-hum
44	466	65.5	1027	24	ABQ54438	Human ovarian anti
45	465.6	65.5	849	22	AAH98186	Human EST-derived

ALIGNMENTS

RESULT 1
AAV35488
ID AAV35488 standard; DNA; 711 BP.
XX AC
XX AAV35488;
XX AC
XX 29-SEP-1998 (first entry)
XX DE
XX Macaque primatized 16C10 light chain DNA.
XX DE
XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
KW immunogen; anti-idiotype reagent; interleukin-2; Igc; immunoglobulin G;
KW T cell proliferation; ss.
XX OS
XX Macaca fascicularis.
XX FH
XX Key Location/Qualifiers
XX CDS 1..711
XX FT /*tag= a
XX FT /product= 16C10 light chain
XX FT
XX PN WO9819706-A1.
XX PD 14-MAY-1998.
XX XX
XX PF 29-OCT-1997; 97MO-US19906.
XX XX
XX PR 08-NOV-1996; 96US-0746361.
XX XX
XX PA (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Brans P, Hanna N;
 XX WPI; 1998-286601/25.
 DR P-PSDB; AAW63764.
 XX
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 XX Example 7; Fig 5a; 87pp; English.
 XX
 CC This sequence encodes a primatized form of the antibody 16C10 light chain
 CC from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotype reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 XX Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;
 SQ

Query Match 100.0%; Score 711; DB 19; Length 711;
 Best Local Similarity 100.0%; Pred. No. 8.6e-172;
 Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGGCTCTGGCTCCAGGTGACGATGT 60
 DB 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGGCTCTGGCTCCAGGTGACGATGT 60
 QY 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGAGAGGTCCACATC 120
 DB 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGAGAGGTCCACATC 120
 QY 121 TGTGTCACATGGGAGCACCTCCACATTTGGAGGTATGATCTACATTTGACAGAGCTC 180
 DB 121 TGTGTCACATGGGAGCACCTCCACATTTGGAGGTATGATCTACATTTGACAGAGCTC 180
 QY 181 CCAGGAACGGCCCCCAAACTCTCATCTATGACATTAAAGCGACCTCAGGAATTTCT 240
 DB 181 CCAGGAACGGCCCCCAAACTCTCATCTATGACATTAAAGCGACCTCAGGAATTTCT 240
 QY 241 GACCGATTCTGTGGTCCAAAGTCTGTGACCGGGCCCTCCCTGGCCCATCATCTGGTCCAG 300
 DB 241 GACCGATTCTGTGGTCCAAAGTCTGTGACCGGGCCCTCCCTGGCCCATCATCTGGTCCAG 300
 QY 301 ACTGAGGATGAGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTGATGCTCAGGTA 360
 DB 301 ACTGAGGATGAGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTGATGCTCAGGTA 360
 QY 361 TTCGAGGAGGAGACCGGGTCCAGCTCTAGGTTCAGCCCAAGGTCGCCCTCGGTCACT 420
 DB 361 TTCGAGGAGGAGACCGGGTCCAGCTCTAGGTTCAGCCCAAGGTCGCCCTCGGTCACT 420
 QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGTGTGTCTCAT 480
 DB 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGTGTGTCTCAT 480
 QY 481 AGTGACTTCTACCGGGAGCCGTGACAGTGGCTTGAAGGAGATAGAGCCCGTCAAG 540
 DB 481 AGTGACTTCTACCGGGAGCCGTGACAGTGGCTTGAAGGAGATAGAGCCCGTCAAG 540

QY 541 GCGGAGTGGAGACCAACCAACCTCCAAACAAAGCAACAAAGTACGCGCCGACG 600
 DB 541 GCGGAGTGGAGACCAACCAACCTCCAAACAAAGCAACAAAGTACGCGCCGACG 600
 QY 601 TACCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTCA 660
 DB 601 TACCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTCA 660
 QY 661 CATGAAGGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711
 DB 661 CATGAAGGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711

RESULT 2

AAS17246

ID AAS17246 standard; DNA; 711 BP.

XX AAS17246;

AC AAS17246;

XX 12-MAR-2002 (first entry)

DT DNA sequence of a primatized form of the light chain of 16C10 antibody.

XX Human; macaque monkey; light chain; primatized antibody; 16C10 antibody;

KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;

KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;

KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;

KW graft-vs-host disease; immunosuppression; organ rejection;

KW interleukin-2; IL-2; mutant; db.

XX Chimeric - Homo sapiens.

OS Chimeric - Macaca sp.

OS Synthetic.

XX Key Location/Qualifiers

FH 1..711

FT /*tag= a

FT /product= "Light chain of 16C10 antibody"

XX WO200189567-A1.

XX 29-NOV-2001.

XX 22-MAY-2001; 2001WO-US16364.

XX 22-MAY-2000; 2000US-0576424.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Hanna N, Brans P;

XX WPI; 2002-089895/12.

XX P-PSDB; AAW11645.

XX Use of monoclonal antibody which specifically binds to B7.1 antigen

XX CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,

XX treating cancer, graft-vs-host disease and autoimmune disease such as

XX allergy

XX Example 8; Fig 5a; 89pp; English.

XX The present invention relates to a new use of a monoclonal antibody

XX which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen

XX (CD86) for inducing the apoptosis of B7+ cells. The invention is

XX useful for treating diseases such as B cell cancer, lymphoma, a

XX cancer where B cells promote the growth and/or metastasis of tumours,

XX B cell lymphoma, B cell leukaemia, and autoimmune diseases such as

XX idiopathic thrombocytopenia purpura, systemic lupus, erythematosis,

XX type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic

XX anaemia, inflammatory bile disease, allergy, multiple sclerosis

XX or graft-vs-host disease. The antibody is useful for immunosuppression

XX in a human or animal and for treating or preventing resistance to or

```
CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present nucleic
CC acid sequence encodes the light chain of 16C10, a primatised antibody
CC used in the invention to induce apoptosis and inhibit production of
CC interleukin-2 (IL-2).
XX
SQ Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;

Query Match          100.0%; Score 711; DB 24; Length 711;
Best Local Similarity 100.0%; Pred. No. 8.6e-172;
Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGGTCTCTGCTCTCCAGGTCCAGCATGT 60
DB 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGGTCTCTGCTCTCCAGGTCCAGCATGT 60

QY 61 GAGTCTGTCTACACAGCGCCCTCAGTGTCTGGGGCCCGAGGAGAGGTCCACATC 120
DB 61 GAGTCTGTCTACACAGCGCCCTCAGTGTCTGGGGCCCGAGGAGAGGTCCACATC 120

QY 121 TCGTCACCTGGGAGCAGCTCCAACTTGGAGGTATGATCTACATTGGTACCAGCAGTCT 180
DB 121 TCGTCACCTGGGAGCAGCTCCAACTTGGAGGTATGATCTACATTGGTACCAGCAGTCT 180

QY 181 CCAGGAACGGCCCGCCAACTCTCTATGATGATTAACAAGCAGCCCTCAGGAATTTCT 240
DB 181 CCAGGAACGGCCCGCCAACTCTCTATGATGATTAACAAGCAGCCCTCAGGAATTTCT 240

QY 241 GACCGATTCTCTGGTCCCAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGCTCCAG 300
DB 241 GACCGATTCTCTGGTCCCAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGCTCCAG 300

QY 301 ACTGAGGATGAGGCTGATTAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360
DB 301 ACTGAGGATGAGGCTGATTAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360

QY 361 TTCGGAGGAGGACCGGCTGACCGTCTAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 420
DB 361 TTCGGAGGAGGACCGGCTGACCGTCTAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 420

QY 421 CTGTTCCCGCCCTCTCTGAGAGGCTTCAAGCCAAAGGCAACAAAGTACCGGCTGATCTCATA 480
DB 421 CTGTTCCCGCCCTCTCTGAGAGGCTTCAAGCCAAAGGCAACAAAGTACCGGCTGATCTCATA 480

QY 481 ACTGACTTCTACCGGAGCCCTGACAGTGGCTGGAAGGAGATAGAGCCCGCTCAG 540
DB 481 ACTGACTTCTACCGGAGCCCTGACAGTGGCTGGAAGGAGATAGAGCCCGCTCAG 540

QY 541 GCGGAGGTGGAGACCAACACCTCTCAAAACAAAGCAACAAAGTACCGGCTCAGCAGC 600
DB 541 GCGGAGGTGGAGACCAACACCTCTCAAAACAAAGCAACAAAGTACCGGCTCAGCAGC 600

QY 601 TACCTGAGCCTACCGCTGAGCAGTGGAGTCCACAGAGCTACAGTGGCCAGGTTCAG 660
DB 601 TACCTGAGCCTACCGCTGAGCAGTGGAGTCCACAGAGCTACAGTGGCCAGGTTCAG 660

QY 661 CATGAAGGAGACCGTGGAGAGACAGTGGCCCTTACAGATGTTCTATGA 711
DB 661 CATGAAGGAGACCGTGGAGAGACAGTGGCCCTTACAGATGTTCTATGA 711

RESULT 3
AAT62512
ID AAT62512 standard; DNA; 711 BP.
XX
XX AAT62512;
XX
XX 25-MAY-1997 (first entry)
XX
XX Primatised anti-human B7.1 antigen antibody 16C10 light chain DNA.
```

```
XX Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic rheumatoid arthritis; psoriasis;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma; ss.
XX
XX Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
XX WO9640878-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US10053.
XX
XX 07-JUN-1995; 95US-0487550.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX
XX WPI; 1997-108638/10.
XX
XX P-PSDB; AAW01821.
XX
XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
XX useful for treating autoimmune disease or graft-versus-host disease
XX
XX Claim 11; Fig 10A; 81pp; English.
XX
XX 2 DNA sequences (AAT62512 and AAT62513) respectively code for
XX primatised forms (AAW01821 and AAW01822) of the light and heavy chains
XX of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
XX 16C10. Cloned 16C10 light and heavy variable genes are inserted
XX into an expression vector (pref. NEOSPLA) which contains human light
XX and heavy chain constant region genes to allow prodn. of primatised
XX antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
XX antibodies have also been produced (see also AAW01817-20). The
XX primatised antibodies inhibit the B7:CD28 pathway, making them
XX useful immunosuppressants for the treatment of autoimmune disorders
XX and graft-versus-host disease.
XX
XX Sequence 711 BP; 161 A; 226 C; 193 G; 131 T; 0 other;

Query Match          99.8%; Score 709.4; DB 18; Length 711;
Best Local Similarity 99.9%; Pred. No. 2.2e-171;
Matches 710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGCTCTCCAGGTCCAGCATGT 60
DB 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGCTCTCCAGGTCCAGCATGT 60

QY 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGAGAGGTCCACATC 120
DB 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGAGAGGTCCACATC 120

QY 121 TCGTCACCTGGGAGCAGCTCCAACTTGGAGGTATGATCTACATTGGTACCAGCAGTCT 180
DB 121 TCGTCACCTGGGAGCAGCTCCAACTTGGAGGTATGATCTACATTGGTACCAGCAGTCT 180

QY 181 CCAGGAACGGCCCGCCAACTCTCTATGATGATTAACAAGCAGCCCTCAGGAATTTCT 240
DB 181 CCAGGAACGGCCCGCCAACTCTCTATGATGATTAACAAGCAGCCCTCAGGAATTTCT 240

QY 241 GACCGATTCTCTGGTCCCAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGCTCCAG 300
DB 241 GACCGATTCTCTGGTCCCAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGCTCCAG 300

QY 301 ACTGAGGATGAGGCTGATTAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360
DB 301 ACTGAGGATGAGGCTGATTAATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 360
```

QY 361 TTCCGAGGAGGACCCGGCTGACCGTCTTAGGTACGCCCAAGGCTCCCCCTCGGTCACT 420
 Db 361 TTCCGAGGAGGACCCGGCTGACCGTCTTAGGTACGCCCAAGGCTCCCCCTCGGTCACT 420
 QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTCTCATA 480
 Db 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTCTCATA 480
 QY 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCAGATAGACGCCCGTCAAG 540
 Db 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCAGATAGACGCCCGTCAAG 540
 QY 541 GCGGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
 Db 541 GCGGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
 QY 601 TACCTGAGCTGACGCTGAGCAGTGGAGTGGCCCTTACAGAGTGTTCATGA 711
 Db 601 TACCTGAGCTGACGCTGAGCAGTGGAGTGGCCCTTACAGAGTGTTCATGA 711
 QY 661 CATGAAGGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAGTGTTCATGA 711
 Db 661 CATGAAGGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAGTGTTCATGA 711

RESULT 4

AA03609
 ID AAC66525 standard; cDNA; 935 BP.

XX AAC66525;

XX 15-FEB-2001 (first entry)

XX Human immune system associated protein HISAP-7 coding sequence.

XX Human; immune system associated protein; HISAP-7; immune disorder;

KW infection; autoimmune disease; cancer; ss.

XX Homo sapiens.

XX US6135941-A.

XX 24-OCT-2000.

XX 27-MAR-1998; 98US-0049672.

XX 27-MAR-1998; 98US-0049672.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;

PI Hillman JL, Au-Young J;

XX WPI; 2001-030926/04.

DR P-PSDB; AAB36209.

XX New human immune system associated proteins (HISAP) and polynucleotides
 PT encoding the HISAP, useful for diagnosing, treating or preventing
 PT immune or cell proliferative disorders or infections

PS Claim 3; Column 83-84; 54pp; English.

XX The present invention provides the coding and protein sequences for a
 CC number of human immune system associated proteins (HISAPs). These can be
 CC used in the diagnosis and treatment of various autoimmune disorders,
 CC infections and cell proliferation diseases. The diseases include AIDS,
 CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
 CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
 CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
 CC erythematosus, arteriosclerosis, cirrhosis and cancer.

XX Sequence 935 BP; 216 A; 299 C; 248 G; 172 T; 0 other;

Query Match 81.9%; Score 582.6; DB 22; Length 935;
 Best Local Similarity 89.8%; Pred. No. 5.2e-139;
 Matches 637; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

QY 4 AGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCAGGTGCGAGTGTGAG 63
 Db 74 ATGGCTCGTCTCCTCTCCTCTCCTCACTCTCCTCGCTCACTGTCACAGGGTCTCTGGGCCAG 133
 QY 64 TCTGTCTTCGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGCGCAAGGTGACCATCTCG 123
 Db 134 TCTGTCTTCGACAGCGCCCTCAGTGTCTGGGGCCCGAGGCGAGGGTCAACATCTCC 193
 QY 124 TGCACCTGGGAGCACCTCCCAACATTGG---AGGTATATGATCTACATTTGTTACAGAGCTC 180
 Db 194 TGCACCTGGGAGCACCTCCCAACATTGGGGGAGGTTATGATGTACACTGTGTACAGAGCTT 253
 QY 181 CGAGGAACGGGCCCCCAAACTCTCTATCTATGACATTAACAAGCGACCTCTAGGAATTTCT 240
 Db 254 CGAGGAACAGCCCCCAAACTCTCTATCTATGATGTAGAAAATCGGCCCTCTAGGGGTCTCCT 313
 QY 241 GACGATTTCTCTGGCTCCAAAGTCTGGTACCGGGCTCCCTGGCCCATCACTGGGCTCCAG 300
 Db 314 GACGATTTCTCTGGCTCCAAAGTCTGGTACCGGGCTCCCTGGCCCATCACTGGGCTCCAG 373
 QY 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTTATGACAGCAGCTCTGAAATGCTCAGSTA 360
 Db 374 GCTGAGGATGAGGCTGATTATTACTGCCAGTCTTATGACAGCAGCTCTGAGTGTGTA 433
 QY 361 TTCCGAGGAGGACCCGGCTCCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 420
 Db 434 TTCCGAGGAGGACCCAGCTGACCGTCTCTCGGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 493
 QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTCTCATA 480
 Db 494 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACACTGGTGTCTCATA 553
 QY 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCAGATAGCAGGCCCTCAAG 540
 Db 554 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGCAGATAGCAGGCCCTCAAG 613
 QY 541 GCGGGAGTGGAGACCAACACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
 Db 614 GCGGGAGTGGAGACCAACACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 673
 QY 601 TACCTGAGCTGAGCGCTGAGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 660
 Db 674 TACCTGAGCTGAGCGCTGAGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 733
 QY 661 CATGAAGGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAGTGTTCAT 709
 Db 734 CATGAAGGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAGTGTTCAT 782

RESULT 5

AA03609

ID AA03609 standard; cDNA; 884 BP.

XX AA03609;

XX 06-AUG-1989 (first entry)

XX Sequence encoding 4G12 monoclonal antibody (Mab) L chain.

XX 4G12 Mab; human lung cancer; oesophageal carcinoma; ss.

XX Synthetic.

XX Location/Qualifiers

XX Key 25..729

XX CDS /tag= a

XX product=4G12 L

XX 25..375

XX misc_feature /tag= b

	Matches	610;	Conservative	0;	Mismatches	53;	Indels	3;	Gaps	1
Qy	47	CAGGTGACAGTGTGAGTCTGTCGACACAGCGCGCCTCAGTGTCTGGGGCCCCCAGGGC	106							
Db	70	CAGGTGTCACCTCCACGTCGTGTTGACGACGAGCGCCCTCAGTCTCTGCGGCCCCAGGAC	129							
Qy	107	AGNAGTGCACCATCTCGTGCACTGGGAGCACCTCGAACATTGG---AGGTTATGATCTAC	163							
Db	130	AGAAGGTGCAACCATCTCTGTCGACTGGGAGCAGCTCCAACTCGGGGCGAGGTTATGATGTTCT	189							
Qy	164	ATTGGTGACGACGAGTCCCGAGGACGGCCCCCAAACTCCTCATCTATGACATTAAACAAGC	223							
Db	190	ACTGTTACCGGCAATTCACGGGACAGCCCCCAAACTCCTCATCTATGATAAACAACTC	249							
Qy	224	GACCCCTCAGGAATTTCTGACCGATTTCTCTGGCTCCAAAGTCTGGTACGCGGCCCTCCCTGG	283							
Db	250	GGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCCCTCAGCCTCCCTGG	309							
Qy	284	CAATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCCTATGACAGCA	343							
Db	310	CCATCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCCTATGACAGCA	369							
Qy	344	GCCTGAATGCTCAGGTATTTCCGAGGAGGAGACCCGGCTGACCGTCTTAGGTGAGCCCAAG	403							
Db	370	GCCTGAATGGTTATGTTCTTCGGAACCTGGGACCCAGCTCACCGTCTTAGGTGAGCCCAAG	429							
Qy	404	CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAAGGCCA	463							
Db	430	CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAAGGCCA	489							
Qy	464	CATCGTGTGTCCTATAAGTGACTTCTACCGGGAGCCGTGACAGTGGCCCTGGAAGCGAG	523							
Db	490	CACCTGGTGTGTCCTATAAGTGACTTCTACCGGGAGCCGTGACAGTGGCCCTGGAAGCGAA	549							
Qy	524	ATAGACGCCCTGTAAGCGGGAGGTGGAGACCAACACCCCTCCAAACAAGCAACAACA	583							
Db	550	TTAGCAGCCCCCTCAAGCGGGAGGTGGAGACCAACACCCCTCCAAACAAGCAACAACA	609							
Qy	584	AGTAGCGGCCGACGAGCTACCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCT	643							
Db	610	AGTAGCGGCCGACGAGCTATCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCT	669							
Qy	644	ACAGTGTCCAGGTACGCGATGAAGGGAGCACCGGTGGAGAGACAGTGGGCCCTTACAGAA	703							
Db	670	ACAGTGTCCAGGTACGCGATGAAGGGAGCACCGGTGGAGAGACAGTGGGCCCTTACAGAA	729							
Qy	704	GTTCAT-709								
Db	730	GTTCAT-735								

RESULT 7	
AAC84207	
ID	AAC84207 standard; DNA; 5679 BP.
XX	
AC	AAC84207;
XX	
DT	19-MAR-2001 (first entry)
XX	
DE	Plasmid Glambda-lapcn DNA sequence.
XX	
KW	Monoclonal antibody; F protein; respiratory syncytial virus; RSV;
KW	Glambda-I; human; virucide; RSV propagation; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200069462-A1.
XX	
PD	23-NOV-2000.
XX	
PF	18-MAY-2000; 2000WO-US13694.
XX	
PR	18-MAY-1999; 99US-0134702.

(SMIK) SMITHKLINE BEECHAM CORP.
Gross MS, Sweet RW, Taylor G;
WPI; 2001-024947/03.
Human monoclonal antibody and functional fragments, useful for
therapeutic and/or prophylactic treatment of respiratory syncytial
virus infection, is specifically reactive with the F protein epitope of
the virus -
Claim 6; Fig 9A-E; 102pp; English.
The invention provides a human monoclonal antibody (I) and its functional
fragments specifically reactive with an F protein epitope of respiratory
syncytial virus (RSV), and capable of neutralizing infection by the virus
such as Glambda-1A or Glambda-1B. The antibody can be expressed by
standard recombinant methodology. (I) is useful for detecting RSV by
contacting a source suspected of containing RSV with (I) and determining
whether (I) binds to the source. (I) is also useful for providing passive
immunotherapy prophylactically, to RSV disease in a human. (I) is useful
for therapeutic and/or prophylactic treatment of RSV infection in human
patients, particularly infants and young children. (I) is also useful
as a diagnostic reagent for the determination of RSV mediated disorders
or for tracking progress of treatment of the disorders. The present
sequence represents the continuous DNA sequence of the expression plasmid
Glambda-1Apac containing the RSV neutralising human Glambda-1 mab for the
light chain.

Query Match	78.6%	Score 558.8	DB 22	Length 5679
Best Local Similarity	91.0%	Pred. No. 9.5e-133		
Matches 606	Conservative 0	Mismatches 57	Indels 3	Gaps 1
QY	47	CAGGTGACGATGTGAGTCTGTCTCTACACAGCGCGCCCTCAGTGTCTGGGGCCCCAGGCG	106	
DB	1052	CAGCTACAGGTGCCACTCCGAGCTCAGCAGCGCGCCCTCAGTCTCTGGCGGCCCAAGGAC	1111	
QY	107	AGAAGGTCAACCATCTCGTGCATCTGGGAGCACCTCCAAACATTGG--AGGTTATGATCTAC	163	
DB	1112	AGAAGGTCAACCATCTCTGCATCTGGGAGCAGCTCCAACTCTGGGGCAGGTTATGATGTTCT	1171	
QY	164	ATTGGTACAGCAGCTCCACAGGAACGGCCCCAAAATCTCTATCTATGACATTAAACAAGC	223	
DB	1172	ACTGGTACCGGGAATCTTCAGGGACACGCCCAAACTCCTCATCTATGATAAACAACAATC	1231	
QY	224	GACCCCTCAGGAATTTCTGACCGATCTCTGGCTCCAAAGTCTGTGTACCGGGCCCTCCCTGG	283	
DB	1232	GGCCCTCAGGGTCCCTGACCGAATCTCTGGCTCCAAGTCTGGCCCCCTCAGCCTCCCTGG	1291	
QY	284	CCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCA	343	
DB	1292	CCATCTCTGGCTCCAGGCTGAGGATGAGCTGATTATTACTGCCAGTCTCTATGACAGCA	1351	
QY	344	GCCTGAATGCTCAGGTATTTCGAGGAGGAGGCCGGGCTGACCGTCTTAGGTTCAGCCCAAGG	403	
DB	1352	GCCTGAATGTTATGTCTTCGGAACTGGGACCCAGCTCACCGTCTTAGGTTCAGCCCAAGG	1411	
QY	404	CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAAGSCCA	463	
DB	1412	CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAAGSCCA	1471	
QY	464	CACGTGTGTCTCATPAAGTGAATCTTACCCGGAGCCGTGACAGTGGCTCTGGAAGGCAG	523	
DB	1472	CACGTGTGTCTCATPAAGTGAATCTTACCCGGAGCCGTGACAGTGGCTCTGGAAGGCAG	1531	
QY	524	ATAGCAGCCCGCTCAAGCGGGAGTGGAGACACCAACCACTCCCAACAACAAGCAACA	583	
DB	1532	TTAGCAGCCCGCTCAAGCGGGAGTGGAGACCAACCACTCCCAACAACAAGCAACA	1591	
QY	584	AGTACCGGGCAGCAGCTACTTGAGCCTGAGCAGTGTGGAAGTCCACAGAAAGT	643	

Db 1592 AGTACGGCCAGCAGCTATCTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAAGGT 1651
Qy 644 ACAGCTGCCAGCTCAGCATGAAGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGAAT 703
Db 1652 ACAGCTGCCAGCTCAGCATGAAGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGAAT 1711
Qy 704 GTTCAT 709
Db 1712 GTTCAT 1717

RESULT 8

AA06953
ID AAX06953 standard; DNA; 768 BP.

AC AAX06953;

DT 10-MAY-1999 (first entry)

Monoclonal antibody 4B5 light chain variable region DNA.

KW Antigen binding fragment 4B5; monoclonal antibody; cancer;
KW neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
KW sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;
KW GD2 antigen; human; ds.

OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 19..726
FT /tag= a

PN WO9902545-A2.

XX 21-JAN-1999.

PF 08-JUL-1998; 98WO-IB01046.

PR 08-JUL-1997; 97US-0051945.

PA (NOVO-) NOVOPHARM BIOTECH INC.

XX Dan MD;

PI WPI; 1999-120769/10.

DR P-PSDB; AAW88465.

XX New antibody 4B5 polynucleotides and polypeptides - used to develop
PT products for the diagnosis and treatment of cancers and for
PT prophylactic therapy to reduce risk of recurrence

XX Claim 4; Page 80; 83pp; English.

XX This is the DNA sequence of a polynucleotide that encodes the light
CC chain variable region (see AAW88465) of the recombinant human
CC monoclonal antibody (WAB) 4B5. 4B5 recognises antibodies specific
CC for GD2 antigen antibodies. Antibodies specific for GD2 recognise
CC various cancers including glioblastoma, neuroblastoma, malignant
CC and/or metastatic melanoma, breast adenocarcinoma, lung
CC adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives
CC with immunologic specificity for antibodies specific for GD2. These
CC derivatives, or antigen binding fragments, comprise regions of the
CC 4B5 VDJ junction and regions spanning the 4B5 CDRs. Other
CC derivatives include Fab, Fab', scFv and isolated heavy and
CC light chains. Polynucleotide fragments (see AAX06951-54), both
CC coding and complementary strands, encoding 4B5 antibody V regions
CC are also provided, as well as therapeutic plasmids and vectors,
CC including vaccinia virus vectors, comprising these polynucleotides.
CC 4B5 has been shown to mimic GD2, and is particularly useful in
CC generating a host immune response to cancer. Products of the
CC invention can be used in the detection and treatment of e.g.

CC astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
CC primitive neural ectodermal tumour (PNET), pancreatic ductal
CC adenocarcinoma, small and large cell lung adenocarcinomas,
CC squamous cell carcinoma, bronchoalveolar carcinoma, epithelial
CC adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma,
CC breast tumours such as ductal and lobular adenocarcinoma, squamous
CC and adenocarcinomas of the uterine cervix, uterine and ovarian
CC epithelial carcinoma, prostatic adenocarcinoma, transitional
CC squamous cell carcinoma of the bladder, B and T cell lymphoma
CC (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
XX
SQ Sequence 768 BP; 169 A; 256 C; 202 G; 141 T; 0 other;

Query Match 77.7%; Score 552.6; DB 20; Length 768;

Best Local Similarity 89.6%; Pred. No. 2.2e-131;

Matches 594; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 47 CAGGTGCAGATGTGAGTCTCTGACACAGCCGCCCTCAGTCTCTGGGGCCCCAGGCG 106

Db 62 CAGGGTCTCTGGGCCAGCTCTGTGCTGACTCAGCCACCCCTCAGCGTCTGGGACCCCGGGC 121

Qy 107 AGAAGGTCAACATCTCGTGCACTGGGAGCACCTCCAAACATTGGAGTTATGATCTACATT 166

Db 122 AGAGGTCAACATCTCTTGTCTGGAAGCACTCCAAACATCGGAAGTAAGACTGTAACT 181

Qy 167 GGTACACAGCAGCTCCAGGAAGCGGCCCAAACTCTCATCTATGACATTAACAAGCGAC 226

Db 182 GGTACACAGCAACTCCAGGAAGCGGCCCAAAATTTCTCATCTATGATTAATATCAGCGGC 241

Qy 227 CCTCAGGAATTTCTGACCGATTTCTTGGCTCCAGTCTGGTACCGGGCTCTCCCTGGCCA 286

Db 242 CCTCAGGGGTCTCTGACCGATTTCTTGGCTCCAGTCTGGTACCGGGCTCTCCCTGGCCA 301

Qy 287 TCACCTGGGCTCCAGACTGAGGATGAGGTGATTATTACTGCCAGTCTTATGACAGCAGCC 346

Db 302 TCAGTGGGCTCCAGTCTGAGGATGAGGTGATTATTACTGTCAGATGGATGACAGCC 361

Qy 347 TGAATGCTCAGGTATTTCGGAGGAGGAGCCCGGCTGACCGTCTTAGGTTCAGCCCAAGGCTG 406

Db 362 TGAATGGTTGGGTGTTTCGGGAGGAGCAACAGCTCAGCGTCTGGGTTCAGCCCAAGGCTG 421

Qy 407 CCCCCCTCGGTCACTCTGTTTCCCGCCCTCTCTGAGGAGTTCAGGCCAACAGGCCACAC 466

Db 422 CCCCCCTCGGTCACTCTGTTTCCCGCCCTCTCTGAGGAGTTCAGGCCAACAGGCCACAC 481

Qy 467 TGGTGTGTCTCATAAGTGAATCTTACCCGGGAGCGGTGACAGTGGCGTGGAGGAGGAGATA 526

Db 482 TGGTGTGTCTCATAAGTGAATCTTACCCGGGAGCGGTGACAGTGGCGTGGAGGAGGAGATA 541

Qy 527 GCAGCCCCGTCAAGCGGGAGTGGAGACCAACACACCCCTCCAAACAAAGCAACAAGT 586

Db 542 GCAGCCCCGTCAAGCGGGAGTGGAGACCAACACACCCCTCCAAACAAAGCAACAAGT 601

Qy 587 AGCGGGCCAGCAGTACTTACCTGAGCCTGAGCCTGAGCAGTGGAGTCCCAAGAAGCTACA 646

Db 602 AGCGGGCCAGCAGTACTTACCTGAGCCTGAGCCTGAGCAGTGGAGTCCCAAGAAGCTACA 661

Qy 647 GCTGCCAGGTCAAGCAGTGAAGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGAATGTT 706

Db 662 GCTGCCAGGTCAAGCAGTGAAGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGAATGTT 721

Qy 707 CAT 709

Db 722 CAT 724

RESULT 9

AA06954/c

ID AAX06954 standard; DNA; 768 BP.

XX AAX06954;

XX

DT 10-MAY-1999 (first entry)
 XX Monoclonal antibody 4B5 light chain variable region DNA.
 XX
 KW Antigen binding fragment 4B5; monoclonal antibody; cancer;
 KW neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
 KW sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;
 KW GD2 antigen; human; ds.
 XX
 XX Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS complement (43..750)
 FT /*tag= a
 XX
 PN WO9902545-A2.
 XX
 PD 21-JAN-1999.
 XX
 PF 08-JUL-1998; 98WO-IB01046.
 XX
 PR 08-JUL-1997; 97US-0051945.
 XX
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 PI Dan MD;
 DR WPI; 1999-120769/10.
 XX
 DR P-PSDB; AAW88465.
 XX
 XX New antibody 4B5 polynucleotides and polypeptides - used to develop
 PT products for the diagnosis and treatment of cancers and for
 PT prophylactic therapy to reduce risk of recurrence
 XX
 XX Claim 6; Page 80; 83pp; English.
 XX
 CC This is the complementary strand of a DNA sequence (see also
 CC AAX06953) that encodes the light chain variable region (see AAW88465)
 CC of the recombinant human monoclonal antibody (MAB) 4B5. 4B5
 CC recognises antibodies specific for GD2 antigen antibodies. Such
 CC antibodies recognise various cancers including glioblastoma,
 CC neuroblastoma, malignant and/or metastatic melanoma, breast
 CC adenocarcinoma, lung adenocarcinoma, small cell lung carcinoma,
 CC colon adenocarcinoma and prostate adenocarcinoma. The invention
 CC encompasses 4B5 derivatives with immunologic specificity for
 CC antibodies specific for GD2. These derivatives, or antigen binding
 CC fragments, may comprise regions of the 4B5 VDJ junction and regions
 CC spanning the 4B5 CDRs. Other derivatives include Fab, Fab'12,
 CC Fab', scFv and isolated heavy and light chains. Polynucleotide
 CC fragments (see AAX06951-54), both coding and complementary strands,
 CC encoding 4B5 antibody V regions are also provided, as well as
 CC therapeutic plasmids and vectors, including vaccinia virus vectors,
 CC comprising these polynucleotides. 4B5 mimics GD2, and is useful in
 CC generating a host immune response to cancer. Products of the
 CC invention can be used in the detection and treatment of e.g.
 CC astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
 CC primitive neural ectodermal tumour (PNET), pancreatic ductal
 CC adenocarcinoma, small and large cell lung adenocarcinomas,
 CC squamous cell carcinoma, bronchoalveolar carcinoma, epithelial
 CC adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma,
 CC breast tumours such as ductal and lobular adenocarcinoma, squamous
 CC and adenocarcinomas of the uterine cervix, uterine and ovarian
 CC epithelial carcinoma, prostatic adenocarcinoma, transitional
 CC squamous cell carcinoma of the bladder, B and T cell lymphoma
 CC (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
 CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
 XX
 SQ Sequence 768 BP; 141 A; 202 C; 256 G; 169 T; 0 other;
 Query Match 77.7%; Score 552.6; DB 20; Length 768;
 Best Local Similarity 89.6%; Pred. No. 2.2e-131; Indels 0; Gaps 0;
 Matches 594, Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 47 CAGGTGCACGATGTGAGTCTGCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGC 106
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 648
 QY 107 AGAAGGTACCATCTCGTGCACCTGGGAGCAGCTCCAAATTTGGAGGTTATGATCTACATT 166
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 588
 QY 167 GGTACACGAGCTCCAGGAAACGGCCCAAACTCTCATCTATGACATTAAACAGCGAC 226
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 528
 QY 227 CCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAAGTCTGGTACCGCGGCTCTCCCTGGCCA 286
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 468
 QY 287 TCACGTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCTTATGACAGGAGCC 346
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 408
 QY 347 TGAATGCTCAGTATTTCGGAGGAGGACCCGCTGACCGTCTTAGTCTCAGCCCAAGGGCTG 406
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 348
 QY 407 TGAATGCTGAGTATTTCGGAGGAGGACCCGCTGACCGTCTTAGTCTCAGCCCAAGGGCTG 466
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 288
 QY 467 TGGTGTGCTCATAGTCACTTTACCCGGGAGCGCTGACAGTGGCCCTGGAGGAGGAGATA 526
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 228
 QY 527 GCGAGCCCGCTCAAGCGGGAGTGGAGACCAACACACCTCCAAACAAAGCAACCAAGT 586
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 168
 QY 587 ACGCGGCGAGCTACTGAGCCCTGACCGCTGAGCAGTGGAGTCCACAGAACTACA 646
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 108
 QY 647 GCTGCGAGTCAAGCGGAGGAGCAGCGTGGAGAACACAGTGGCCCTTACAGAAATGTT 706
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 48
 QY 707 CAT 709
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 47 CAT. 45
 RESULT 10
 ID AAO49835
 AC AAO49835 standard; cDNA, 654 BP.
 XX AAO49835;
 DT 27-APR-1994 (first entry)
 XX
 DE Anti-HIV-1 recombinant antibody 447-52D light chain coding sequence.
 KW Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
 KW HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
 KW acquired immune deficiency syndrome; chimeric antibody;
 XX surface glycoprotein gp120; V3 loop; ss.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..654
 FT /*tag= a
 FT /note= "encodes recombinantly modified 447-52D
 light chain"
 XX
 PN WO9319785-A.

XX PD 14-OCT-1993.
XX PF 23-MAR-1993; 93WO-US02629.
XX PR 01-APR-1992; 92US-0861701.
XX (MERI) MERCK & CO INC.
XX (JOHN/) JOHNSON L S.
XX (PFAR/) PFARR D S.
XX Conley AJ, Emimi EA, Johnson LS, Mark GE, Pfarr DS;
XX WPI; 1993-336600/42.
XX P-PSDB; AAR42163.
XX New recombinant human antibody - with HIV neutralising activity
XX against at least two isolates, useful for preventing or treating
XX infection in diagnosis, etc.
XX Example 9; Fig 2B; 154pp; English.
XX EBV-transformed cell lines and mouse-human heterohybridomas
XX producing human WABs specific for the gp120 V3 loop of HIV-1 MN
XX isolate were obtained. WAB 447-52D was found to recognise the
XX tetrapeptide motif GPR, i.e. the Principal Neutralising
XX Determinant common to the V3 loop of different HIV isolates.
XX A recombinant Ab was produced in which the L chain V region was
XX derived from 447-52D and to which a signal sequence and a L chain
XX intronic sequence are appended, fused to a fragment contg. a short
XX lambda 2 constant encoding domain.
XX Sequence 654 BP; 156 A; 199 C; 178 G; 121 T; 0 other;
SQ

Query Match 76.9%; Score 547; DB 14; Length 654;
Best Local Similarity 91.1%; Pred. No. 5.8e-130;
Matches 593; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

QY 62 AGTCTGTCTCTACACAGCGCCCTCAGTGTCTGGGCCCCCAGGAGGTCCACCATCT 121
DB 2 AGTCTGTGTGACGAGCGCCCTCAGTGTCTGGGCCCCCAGGAGGTCCACCATCT 61
QY 122 COTGCACTGGGAGCCTCCAACTTGGAGGTATGATCTACATGTTGTACGAGCTCC 181
DB 62 CTTGCTCTGGAAGCAGCTCCAACTTGGAGGTATGATGTTGTACGAGCTCC 121
QY 182 CAGGAACGGCCCCCAACTCTCTATGATTAACAGGACCTCAGGAATTTCTG 241
DB 122 CAGGAACAGCCCCCAACTCTCTATGATTAACAGGACCTCAGGAATTTCTG 181
QY 242 ACCGATTTCTTGCTCCAGTCTGGTACCGCGCCCTCTGCGCATCACTGGGCTCCAGA 301
DB 182 ACCGATTTCTTGCTCCAGTCTGGTACCGCGCCCTCTGCGCATCACTGGGCTCCAGA 241
QY 302 CTGAGGATGAGGTGATTTACTGTCAGTCTCTATGACAGCAGCTGGAATGTCTCA ---GG 358
DB 242 CTGGGAGCAGGCGCGATTTATTCTGCGCAACATGGATAGCGCCTGAGTGTGTTGG 301
QY 359 TATTGAGGAGGAGCCCGGTGACCGTCTAGTTCAGCCCAAGGCTGCCCTCGTGTCA 418
DB 302 TGTTCGGCGGAGGAGCAAGCTGACCGTCTTAAGTCAGCCCAAGGCTGCCCTCGTGTCA 361
QY 419 CTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCCACTGTTGTTCTCA 478
DB 362 CTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCCACTGTTGTTCTCA 421
QY 479 TAAGTGACTTCTACCGGAGCGGTGACAGTGGCCCTGGAGGAGCAGATAGCAGCCCGTCA 538
DB 422 TAAGTGACTTCTACCGGAGCGGTGACAGTGGCCCTGGAGGAGCAGATAGCAGCCCGTCA 481
QY 539 AGCGGGAGTGAGACCAACCACTCTCCAAACAAAGCAACCAAGTACGGCGGCAGCA 598
|||||

Db 482 AGCGGGAGTGGAGACCAACACACCTCCAAACAAAGCAACCAAGTACGGCGGCAGCA 541
QY 599 GCTACTGAGCTGACCGCTGAGCAGTGAAGTCCACAGAGCTTACAGTCCAGGTCA 658
Db 542 GCTATCTGAGCTGACCGCTGAGCAGTGAAGTCCACAGAGCTTACAGTCCAGGTCA 601
QY 659 CGCATGAAGGGAGCACCCTGGAGAGACAGTGGCCCTTACAAATGTTTCAT 709
Db 602 CGCATGAAGGGAGCACCCTGGAGAGACAGTGGCCCTTACAAATGTTTCAT 652

RESULT 11
AAS87270
ID AAS87270 standard; cDNA; 810 BP.
XX
AC AAS87270;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #23074.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG23083.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1; SEQ ID No 23074; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 810 BP; 176 A; 275 C; 211 G; 148 T; 0 other;

Query Match	76.8%;	Score 546.2;	DB 23;	Length 810;
Best Local Similarity	89.0%;	Prod. No. 9.8e-130;		
Matches 590;	Conservative 0;	Mismatches 73;	Indels 0;	Gaps 0;
Qy	47	CAGGTGCACGATGTGAGTCTCTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGGC	106	
Db	49	CAGGGTCTGGGCCCACTCTGTACTGACGAGCACCTCTGAGCTCTGGGACCCCGGGC	108	
Qy	107	AGAGGTCACCATCTCGTGTGCACTGGGAGCACCTCAACATTTGGAGGTTATGATCTACATT	166	
Db	109	AGAGGGTCACAATCTCTGTGTTCTGGAGCAGCTCCACATCGGCACTAATGATGTATACT	168	
Qy	167	GGTACCAGCAGCTCCACGGACGCCCCCAACTCTCATCTATCACATTAACAAAGCAC	226	
Db	169	GGTACCAGCAACTCACAGAACGCCCCCAACTCTCATCTATAGGAATAATCAGGGC	228	
Qy	227	CCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAAGTCTGGTACCGCGGCCCTCCCTGGGCCA	286	
Db	229	CCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCTCTCAGCCTCCCTGGGCCA	288	
Qy	287	TCACTGGGCTCCAGACTGAGGATGAGGCTGATTAATTACTGCCAGTCTCTATGACAGCAGCC	346	
Db	289	TCAGTGGCCTCCAGTCCGAGGATGAGGCTGATTAATTACTGTGCAGCATGGGATGCAGACC	348	
Qy	347	TGAATGCTCAGGTATTTCGGAGGAGGACCCGGCTGACCGTCTAGTTCAGCCCAAGGCTG	406	
Db	349	TCAGTGTGCGGTGTTTCGGGAGGAGGACCAAGCTGACCGTCTAGTTCAGCCCAAGGCTG	408	
Qy	407	CCCCCTCGGTCACCTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACAC	466	
Db	409	CCCCCTCGGTCACCTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACAC	468	
Qy	467	TGTTGTGTCTCAATAGTGACTTTCTACCCGGGAGCGGTGACAGTGGCTTGGAAAGCAGATA	526	
Db	469	TGTTGTGTCTCATAGTGACTTCTTACCCGGGAGCGGTGACAGTGGCTTGGAAAGCAGATA	528	
Qy	527	GCAGCCCGCTCAAGCGGAGGTGAGACCCACACACCTCCAAACAAGCAACCAACAGT	586	
Db	529	GCAGCCCGCTCAAGCGGAGGTGAGACCCACACACCTCCAAACAAGCAACCAACAGT	588	
Qy	587	ACGCGGCCAGCAGCTACTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAGCTACA	646	
Db	589	ACGCGGCCAGCAGCTACTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAGCTACA	648	
Qy	647	GCTGCCAGGTCACGCATGAAGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAATGTT	706	
Db	649	GCTGCCAGGTCACGCATGAAGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAATGTT	708	
Qy	707	CAT 709		
Db	709	CAT 711		
RESULT 12				
AAT62509				
ID ID AAT62509 standard; DNA; 705 BP.				
XX AC AAT62509;				
XX DT 25-MAY-1997 (first entry)				

Prima¹tised anti-human B7.1 antigen antibody 7C10 light chain DNA.

[illegible]

QY 541 GCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAACTACGCGCCAGCAGC 600
 Db 535 GCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAACTACGCGCCAGCAGC 594
 QY 601 TACCTGAGCCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTACG 660
 Db 595 TACCTGAGCCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTACG 654
 QY 661 CATGAAGGGAGCAGCCTGAGAGACAGTGGCCCTACAGATGTTTCATGA 711
 Db 655 CATGAAGGGAGCAGCCTGAGAGACAGTGGCCCTACAGATGTTTCATGA 705

RESULT 13

AAV35484
 ID AAV35484 standard; DNA; 705 BP.

AC AAV35484;

XX 29-SEP-1998 (first entry)

DE Macaque primatized 7C10 light chain DNA.

XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation; ss.

XX Macaca fascicularis.

XX Key Location/Qualifiers
 FT 1..705
 FT CDS /*tag= a
 FT /product= 7C10 light chain

XX W09819706-A1.

XX 14-MAY-1998.

XX 29-OCT-1997; 97WO-US19906.

XX 08-NOV-1996; 96US-0746361.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Brams P, Hanna N;

XX WPI; 1998-286601/25.

XX P-PSDB; AAW63760.

XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 XX cells, e.g. graft rejection or tumours

XX Example 7; Fig 3a; 87pp; English.

XX This sequence encodes a primatized form of the antibody 7C10 light chain
 CC from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotype reagents. Mab's are optionally combined with other proteins

CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.

XX SQ Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match 76.0%; Score 540.2; DB 19; Length 705;
 Best Local Similarity 86.1%; Pred. No. 3.2e-128;
 Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCCAAGGTCCAGATGT 60
 Db 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCCAAGGTCCAGATGT 60
 QY 61 GAGTCTGTCTGACACAGCCGCTCAGTGTCTGGGGCTCCCAAGGTCCAGATGT 120
 Db 61 GCCTATGAATGACTCAGCCACCTCGGTGTCAAGTGTCCCAAGGTCCAGATGT 120
 QY 121 TCGTGCACTGGAGCACCTCCAAATGAGGTATGATCTACATGTGTACAGAGCTC 180
 Db 121 ACCTGTGGGG-----AGACAACAGTAGAATGATATGTCCACTGGTACCAGAGAAG 174
 QY 181 CCAGAAACGGCCCCCAAACTCTCATCTATGACATTAACAGCGACCTCAGATTTCT 240
 Db 175 CCAGCGGGGGCCCCCTATATCTGTATGATAGTACCGGCCCTCAGGGATCCCT 234
 QY 241 GACCATTTCTCTGGCTCCCAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGTCCAG 300
 Db 235 GAGCATTTCTCTGGCTCCCAATCAGGGAACACCGCCACCTTGACCATCAACGGGGTCGAG 294
 QY 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTCTCAGGTA 360
 Db 295 GCGGGGATGAGGCTGACTATTACTGTGCGGACAGGGCTAGTATCATCCGGTC 354
 QY 361 TTGAGGAGGAGACCGGGCTGACCGTCTAGTGTAGCCCAAGGCTGCCCTCGGTCACT 420
 Db 355 TTGAGGAGGAGACCGGGGTGACCGTCTAGGTTCAGCCCAAGGGTGCCTCGGTCACT 414
 QY 421 CTGTTCCCGCTCTCTGAGGAGCTTCAAGCAACAAAGGCCACACTGGTGTCTCATA 480
 Db 415 CTGTTCCCGCTCTCTGAGGAGCTTCAAGCAACAAAGGCCACACTGGTGTCTCATA 474
 QY 481 AGTGACTTTTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAATAGCAGCCCGTCAAG 540
 Db 475 AGTGACTTTTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAATAGCAGCCCGTCAAG 534
 QY 541 GCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGCCAGCAGC 600
 Db 535 GCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGTACGCGCCAGCAGC 594
 QY 601 TACCTGAGCCTGAGCCCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTTCAGC 660
 Db 595 TACCTGAGCCTGAGCCCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTTCAGC 654
 QY 661 CATGAAGGGAGCAGCCTGAGAGACAGTGGCCCTACAGATGTTTCATGA 711
 Db 655 CATGAAGGGAGCAGCCTGAGAGACAGTGGCCCTACAGATGTTTCATGA 705

RESULT 14

AAAS17242

ID AAS17242 standard; DNA; 705 BP.

XX AC AAS17242;

XX 12-MAR-2002 (first entry)

XX DNA sequence of a primatized form of the light chain of 7C10 antibody.

XX Human; macaque monkey; light chain; primatized antibody; 7C10 antibody;
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis;

KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; ds.

XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FT 1..705
 CDS /*tag= a
 FT /product= "Light chain of 7C10 antibody"

XX WO200189567-A1.

XX 29-NOV-2001.

XX 22-MAY-2001; 2001WO-US16364.

XX 22-MAY-2000; 2000US-0576424.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Hanna N, Brans P;

XX WPI; 2002-089895/12.

XX P-PSDB; AAU11538.

XX Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 PT treating cancer, graft-vs-host disease and autoimmune disease as
 PT allergy

XX Example 8; Fig 3a; 89pp; English.

XX The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or
 CC rejection of transplanted organ or tissue for treating proliferative
 CC and hyperproliferative diseases, for treating reversible obstructive
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,
 CC rhinitis and eczema, and other types of allergies. The present nucleic
 CC acid sequence encodes the light chain of 7C10, a primatised antibody
 CC used in the invention to induce apoptosis and inhibit production of
 CC interleukin-2 (IL-2).

XX Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Query Match 76.0%; Score 540.2; DB 24; Length 705;
 Best Local Similarity 86.1%; Pred. No. 3.2e-128;
 Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGGTCCCGGCTCAGCTCTGGGGTCTCTGGCTCCAGGTGCAGATGT 60
 Db |||||
 1 ATGAGGGTCCCGGCTCAGCTCTGGGGTCTCTGGCTCCAGGTGCAGATGT 60
 QY 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGACAGAGTCCCATC 120
 Db |||||
 61 GCCTATGAATGACTCAGCCACCTCGGTGTGAGTGTCCCGAGGACAGCGCCAGGATC 120
 QY 121 TCGTCACTGGGAGCACCTCCAACTTGGAGTTATGATCTACATTGTTACAGCAGCTC 180
 Db |||||
 121 AGCTGTGGGG-----AGACAAAGTAGAATGAATATGTCCCTGGTACCAGAGAAG 174

QY 181 CCAGGAACGGCCCCCAAACTCTCTATCTATGACATTAAACAAGCGACCTCAGGAATTTCT 240
 Db |||||
 175 CCAGCGCGGGCCCCCTATATCTGTCTATCTATGATAGTAGTACCGGCCCTCAGGATCCCT 234
 QY 241 GACCGATTCTCTGGCTCCAAAGTCTGGTACCGGGCTCCCTGGCCATCAGTGGGTCCAG 300
 Db |||||
 235 GAGCGATTCTCTGGCTCCAAATCAGGGAAACACCGCCACCTGACCATCAACGGGGTCGAG 294
 QY 301 ACTGAGGATGAGGTGATTATTACTTGCAGTCTCTATGACAGCAGCCTCAATGCTCAGGTA 360
 Db |||||
 295 GCCGGGATGAGGCTGACTATTACTGTGAGGTGGGACAGGGCTAGTATCATCATCGGTC 354
 QY 361 TTCGAGGAGGAGCCCGGCTGACCGTCTTCTAGTTCAGCCCAAGGCTGCCCCCTCGGTCACT 420
 Db |||||
 355 TTCGAGGAGGAGCCCGGCTGACCGTCTTCTAGTTCAGCCCAAGGCTGCCCCCTCGGTCACT 414
 QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGAGCCACACTGGTGTCTCATATA 480
 Db |||||
 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGAGCCACACTGGTGTCTCATATA 474
 QY 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGCCTGGAAGGAGAGATAGCAGCCCTCAAG 540
 Db |||||
 475 AGTGACTTCTACCCGGGAGCCGTGACAGTGCCTGGAAGGAGAGATAGCAGCCCTCAAG 534
 QY 541 GCGGAGTGGAGACACACACCCCTCCAAACAAAGCAACAAGTACCGCGCCAGCAGC 600
 Db |||||
 535 GCGGAGTGGAGACACACACCCCTCCAAACAAAGCAACAAGTACCGCGCCAGCAGC 594
 QY 601 TACTTGACCTGACCGCTGACAGTGGAGTCCACAGAGCTACAGTCCAGGTCCAG 660
 Db |||||
 595 TACTTGACCTGACCGCTGACAGTGGAGTCCACAGAGCTACAGTCCAGGTCCAG 654
 QY 661 CATGAAGGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCATGA 711
 Db |||||
 655 CATGAAGGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCATGA 705

RESULT 15
 AAV11293

ID AAV11293 standard; cDNA; 651 BP.

XX AAV11293;

XX 27-AUG-1998 (first entry)

DE Antibody HB4C5 light chain encoding cDNA.

XX Antibody light chain; carboxypeptidase; bovine pancreas; cancer;
 KW porcine pancreas; radioimmunoinaging; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT 1..651
 FT /*tag= a
 FT /product= "Antibody HB4C5 light chain"
 FT /note= "the start and stop codons are not indicated"

XX JPI0075791-A.

XX 24-MAR-1998.

XX 30-AUG-1996; 96JP-0246825.

XX 30-AUG-1996; 96JP-0246825.

XX (MOMI) MORINAGA & CO LTD.

XX WPI; 1998-244364/22.

XX P-PSDB; AAU40533.

XX New antibody light chain or its fragment - useful for preparation of
 PT therapeutic(s) or cancer radio-immuno-imaging agent(s)

XX SD

Claim 12; Fig 9; 20pp; Japanese.



CC This cDNA encodes a antibody HB4C5 light chain. This antibody light chain
CC or its fragment is specific for carboxypeptidase from bovine or porcine
CC pancreas and is reactive with human cancer tissue. The antibody light
CC chain and its fragment can be used for preparation of a cancer
CC radioimmunoinaging reagent and therapeutic compositions.

CC radioimmunoimaging reagent and therapeutic compositions.

XX

SQ Sequence 651 BP; 160 A; 207 C; 164 G; 120 T; 0 other;

Query Match 75.0%; Score 533.2; DB 19; Length 651;

Best Local Similarity 89.8%; Pred. No. 1.9e-126;

Matches 584; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY 62 AGTCTGTCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGTCAACATCT 121

Db

2 AGTCTGTGTTGACGAGCGCCCTCAGTGTCTCGGCCCCAGGACAGAAAGTCCACATCT 61

QY 122 CGTGCACTGGGAGCACCTCCAACATTTGGAGGTTATGATCTACATTGGTACCAGCAGCTCC 181

Db 62 CCTGCTCTGGAAACAGCTCCAACATTGGGAATAATTATGTATCTCTGGTACAGACCTCC 121

QY 182 CAGGAACGGCCCCCAAACTCCTCATCTATGACATTAAACAAGCGACCCTCAGGAATTTCTG 241

Db 122 CAGGAACAGCCCCCAACTCTCTCATTTTATGACAAATAATAGCGACCCCTCAGTATTTCCTG 181

242 ACCGATTCTGGCTCCAAGTCTGGTACCGGGCCTCCCTGGGCATCACTGGGCTCCAGA 301

27	ACCGGATCTCTGGCTTCCAAAGTCTGGCAGCGTCTGGCA	CCCTGGGGCAATCACGGACTCCAGA	241
Db	182		
	272		

302 CTGAGGATGAGGCTGATTATTCTGCCAGTCTTATGACAGCAGCCTGAATG---CTCAGG 358

QY	CTGAGGATGAGGCTGATATATACAGCCAGTCCATGACAGGAGCCATGAAATG--CTCAGG	355
302	CTGAGGATGAGGCTGATATATATACAGCCAGTCCATGACAGGAGCCATGAAATG--CTCAGG	355
db	CTGGGACAGGGCCGATTATCTGGGCACATGACTAGCATCTCCGGTCAATTGGC	301
242	CTGGGACAGGGCCGATTATCTGGGCACATGACTAGCATCTCCGGTCAATTGGC	301

0x 359 TATTCCGACCGGACCTCCTAGGTGACCAAGCATCCCCCTGGTGA 418

359	TATTCGAGGAGGAGGACCCGGCTACCGCTCTAGGTCAGCCCAAGGGTTCGCCCCCTCCGCTCA	411
360		
361	TGTTTCGGCGAGGAGGACTAAACCTGACACGTCCTAGCTAGCCCAAGGCTTCGCCCCCTCGCTCA	412
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[illegible][illegible][illegible][illegible]

C

QY	539	AGGCGGAGTGGAGACCA	CACCA	CACCTCCAAACAAAGCA	CAACAAACAGTACGCGGC	GCA	598
QY	402	AGGCGGAGTGGAGACCA <td>CACCA <td>CACCTCCAAACAAAGCA <td>CAACAAACAGTACGCGGC <td>GCA</td> <td>598</td> </td></td></td>	CACCA <td>CACCTCCAAACAAAGCA <td>CAACAAACAGTACGCGGC <td>GCA</td> <td>598</td> </td></td>	CACCTCCAAACAAAGCA <td>CAACAAACAGTACGCGGC <td>GCA</td> <td>598</td> </td>	CAACAAACAGTACGCGGC <td>GCA</td> <td>598</td>	GCA	598

Qy	599	658	723	788	853	918	983	1048	1113	1178	1243	1308	1373	1438	1503	1568	1633	1698	1763	1828	1893	1958	2023	2088	2153	2218	2283	2348	2413	2478	2543	2608	2673	2738	2803	2868	2933	2998	3063	3128	3193	3258	3323	3388	3453	3518	3583	3648	3713	3778	3843	3908	3973	4038	4103	4168	4233	4298	4363	4428	4493	4558	4623	4688	4753	4818	4883	4948	5013	5078	5143	5208	5273	5338	5403	5468	5533	5598	5663	5728	5793	5858	5923	5988	6053	6118	6183	6248	6313	6378	6443	6508	6573	6638	6703	6768	6833	6898	6963	7028	7093	7158	7223	7288	7353	7418	7483	7548	7613	7678	7743	7808	7873	7938	8003	8068	8133	8198	8263	8328	8393	8458	8523	8588	8653	8718	8783	8848	8913	8978	9043	9108	9173	9238	9303	9368	9433	9498	9563	9628	9693	9758	9823	9888	9953	10018	10083	10148	10213	10278	10343	10408	10473	10538	10603	10668	10733	10798	10863	10928	10993	11058	11123	11188	11253	11318	11383	11448	11513	11578	11643	11708	11773	11838	11903	11968	12033	12098	12163	12228	12293	12358	12423	12488	12553	12618	12683	12748	12813	12878	12943	13008	13073	13138	13203	13268	13333	13398	13463	13528	13593	13658	13723	13788	13853	13918	13983	14048	14113	14178	14243	14308	14373	14438	14503	14568	14633	14698	14763	14828	14893	14958	15023	15088	15153	15218	15283	15348	15413	15478	15543	15608	15673	15738	15803	15868	15933	15998	16063	16128	16193	16258	16323	16388	16453	16518	16583	16648	16713	16778	16843	16908	16973	17038	17103	17168	17233	17298	17363	17428	17493	17558	17623	17688	17753	17818	17883	17948	18013	18078	18143	18208	18273	18338	18403	18468	18533	18598	18663	18728	18793	18858	18923	18988	19053	19118	19183	19248	19313	19378	19443	19508	19573	19638	19703	19768	19833	19898	19963	20028	20093	20158	20223	20288	20353	20418	20483	20548	20613	20678	20743	20808	20873	20938	21003	21068	21133	21198	21263	21328	21393	21458	21523	21588	21653	21718	21783	21848	21913	21978	22043	22108	22173	22238	22303	22368	22433	22498	22563	22628	22693	22758	22823	22888	22953	23018	23083	23148	23213	23278	23343	23408	23473	23538	23603	23668	23733	23798	23863	23928	23993	24058	24123	24188	24253	24318	24383	24448	24513	24578	24643	24708	24773	24838	24903	24968	25033	25098	25163	25228	25293	25358	25423	25488	25
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	(c)
	(d)
	(e)
	(f)
	(g)
	(h)
	(i)
	(j)
	(k)
	(l)

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Search completed: June 3, 2003, 14:45:38
Job time : 160.886 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 17:51:01 ; Search time 93.7363 Seconds
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Perfect score: 711
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	711	100.0	711	9	US-09-948-4298-9
3	711	100.0	711	9	US-10-073-138-5
4	552.6	77.7	768	10	US-09-747-669-4
5	552.6	77.7	768	10	US-09-747-669-5
6	552.4	77.4	848	9	US-10-158-646-70
7	550.6	77.4	888	9	US-10-158-646-71
8	540.2	76.0	705	9	US-10-124-905-1
9	540.2	76.0	705	9	US-09-948-4298-1
10	540.2	76.0	705	9	US-10-073-138-1
11	534.8	75.2	2112	9	US-10-001-857-108
12	532.2	74.9	915	10	US-09-954-456-788
13	532.2	74.9	915	10	US-09-880-107-3743
14	504.2	70.9	883	9	US-10-158-646-73
15	484.2	68.1	885	9	US-09-852-797-47
16	484.2	68.1	885	10	US-09-853-161-47
17	484.2	68.1	885	10	US-09-852-659A-47
18	482.6	67.9	879	9	US-09-852-797-29
19	482.6	67.9	879	10	US-09-853-161-29

20	482.6	67.9	879	10	US-09-852-659A-29
21	474	66.7	2667	9	US-10-158-646-76
22	468.4	65.9	702	9	US-10-211-357-5
23	457.6	64.4	960	10	US-09-925-301-582
24	456	64.1	868	10	US-09-822-849A-157
25	449.8	63.3	1480	9	US-09-981-353-146
26	446.8	62.8	2667	9	US-10-158-646-76
27	440.2	61.9	857	10	US-09-822-849A-158
28	429.4	60.4	846	9	US-09-981-353-55
29	422.8	59.5	938	9	US-09-828-995B-25
30	422.8	59.5	938	9	US-09-828-995B-27
31	422.4	59.4	830	9	US-09-981-353-42
32	412	57.9	928	9	US-09-852-797-46
33	412	57.9	928	10	US-09-853-161-46
34	412	57.9	928	10	US-09-852-659A-46
35	411.4	57.9	670	9	US-09-968-433-40
36	410	57.7	611	9	US-09-968-433-36
37	410	57.7	611	9	US-09-968-433-37
38	408	57.4	826	9	US-10-098-841-316
39	405.8	57.1	543	9	US-09-736-457-970
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44	396.6	55.8	5079	10	US-09-809-517A-41
45	394.2	55.4	1480	9	US-09-981-353-146

ALIGNMENTS

RESULT 1
US-10-124-905-9
; Sequence 9, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs

Sequence 29, Appl
Sequence 76, Appl
Sequence 5, Appl
Sequence 582, App
Sequence 157, App
Sequence 146, App
Sequence 76, Appl
Sequence 158, App
Sequence 55, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 42, Appl
Sequence 46, Appl
Sequence 46, Appl
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Sequence 36, Appl
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Sequence 316, App
Sequence 970, App
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Sequence 18, App
Sequence 41, Appl
Sequence 146, App

;; PRIOR APPLICATION NUMBER: US 09/111,286
;; PRIOR FILING DATE: 1998-07-07
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 768
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic construct
US-09-747-669-4

Query Match 77.7%; Score 552.6; DB 10; Length 768;
Best Local Similarity 89.6%; Pred. No. 3.2e-163;
Matches 594; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 47 CAGGTGCACGATGTGAGTCTGCTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGCG 106
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QY 62 CAGGGTCTGGGCCAGTCTGTGCTGACTCAGCCACCTCAGCGTCTGGGACCCCGGCG 121
Db |||||
QY 107 AGAAGGTCAACCATCTCGTGCACCTGGGAGCAGCCTCCAACTTGGAGGTTATGATCTACATT 166
Db |||||
QY 122 AGAGGTCAACCATCTCTGTTCTGGAAGCACTCCCAATCGGAAGTAAAGACTGTAACT 181
Db |||||
QY 167 GGTACAGCAGTCTCCAGGAACGGCCCCAACTCTCTATATGATGACATTAAACAGCGAC 226
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QY 182 GGTACAGCAACTCCAGGAACGGCCCCAACTCTCTATATGATGACATTAAATCAGCGCG 241
Db |||||
QY 227 CCTCAGGAATTTCTGACCATCTCTGGCTCCAGTCTGGTACCGGGCTCCCTGGCCA 286
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QY 242 CCTCAGGGTCTCTGACCATCTCTGGCTCCAGTCTGGTACCGGGCTCCCTGGCCA 301
Db |||||
QY 287 TCATCGGGCTCCAGACTGAGGATGAGCTGATTATTACTGCCAGTCTTATGACAGCAGCC 346
Db |||||
QY 302 TCATCGGGCTCCAGTCTGAGGATGAGCTGATTATTACTGTGCAGATGGGATGACAGCC 361
Db |||||
QY 347 TGAATGCTCAGGTATTCGAGAGGAGCCCGGCTGACCGTCTAGTCTAGCCCAAGGCTG 406
Db |||||
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Db |||||
QY 407 CCGCTCGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 466
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Db |||||
QY 467 TGTGTGTCTCATAGTACTTCTACCGGAGCGGTGACAGTGGCTCGAAGGCGAGATA 526
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Db |||||
QY 527 GCAGCCCGCTCAAGCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAAGT 586
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QY 587 ACAGCGGAGAGCTTACCTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACA 646
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QY 602 ACAGCGGAGAGCTTACCTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACA 661
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QY 707 CAT 709
Db |||||
QY 722 CAT 724
Db |||||

RESULT 5
US-09-747-669-5/c
;; Sequence 5, Application US/09747669
;; Patent No. US20020122807A1
;; GENERAL INFORMATION:
;; APPLICANT: Dan, Michael D.
;; APPLICANT: Saleh, Mansoor
;; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED

;; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
;; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
;; FILE REFERENCE: 316082001001
;; CURRENT APPLICATION NUMBER: US/09/747,669
;; CURRENT FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US 09/111,286
;; PRIOR FILING DATE: 1998-07-07
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5
;; LENGTH: 768
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic construct
US-09-747-669-5

Query Match 77.7%; Score 552.6; DB 10; Length 768;
Best Local Similarity 89.6%; Pred. No. 3.2e-163;
Matches 594; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 47 CAGGTGCACGATGTGAGTCTGCTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGCG 106
Db |||||
QY 707 CAGGGTCTGGGCCAGTCTGTGCTGACTCAGCCACCTCAGCGTCTGGGACCCCGGCG 648
Db |||||
QY 107 AGAAGGTCAACCATCTCGTGCACCTGGGAGCAGCCTCCAACTTGGAGGTTATGATCTACATT 166
Db |||||
QY 647 AGAGGTCAACCATCTCTGTTCTGGAAGCACTCCAACTCGGAAGTAAAGACTGTAACT 588
Db |||||
QY 167 GGTACAGCAGTCTCCAGGAACGGCCCCAACTCTCTATATGATGACATTAAACAGCGAC 226
Db |||||
QY 587 GGTACAGCAACTCCAGGAACGGCCCCAACTCTCTATATGATGACAGCGCG 528
Db |||||
QY 227 CCTCAGGAATTTCTGACCATCTCTGGCTCCAGTCTGGTACCGGGCTCCCTGGCCA 286
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QY 527 CCTCAGGGTCTCTGACCATCTCTGGCTCCAGTCTGGCAGCTTCAAGCCCTCCCTGGCCA 468
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QY 287 TCATCGGGCTCCAGACTGAGGATGAGCTGATTATTACTGCCAGTCTTATGACAGCAGCC 346
Db |||||
QY 467 TCATCGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCC 408
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QY 347 TGAATGCTCAGGTATTCGAGAGGAGGACCCGGCTGACCGTCTTAGGTGAGCCCAAGGCTG 406
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QY 407 TGAATGCTCAGGTATTCGAGAGGAGGACCCAGCTGACCGTCTTAGGTGAGCCCAAGGCTG 348
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Db |||||
QY 347 CCGCTCGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 288
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QY 467 TGTGTGTCTCATAGTACTTCTACCGGAGCGGTGACAGTGGCTCGGAGGCGAGATA 526
Db |||||
QY 287 TGTGTGTCTCATAGTACTTCTACCGGAGCGGTGACAGTGGCTCGGAGGCGAGATA 228
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Db |||||
QY 587 ACAGCGGAGAGCTTACCTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACA 646
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QY 47 CAT 45
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US-10-158-646-70

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: Sequence 70, Application US/10158646A
: Publication No. US20030073105A1
: GENERAL INFORMATION:
: APPLICANT: Lasek, Amy K.W.
: APPLICANT: Sornasse, Thierry
: TITLE OF INVENTION: GENES EXPRESSED
: FILE REFERENCE: PA-0030-1 US
: CURRENT APPLICATION NUMBER: US/10/11
: CURRENT FILING DATE: 2002-05-29
: PRIOR APPLICATION NUMBER: 60/295,233
: PRIOR FILING DATE: 2001-05-31
: NUMBER OF SEQ ID NOS: 78
: SOFTWARE: PERL Program
: SEQ ID NO 70
: LENGTH: 848
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: Incyte ID No. U
US-10-158-646-70

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Best Local Similarity	87.0%;	Pred. No. 3.7e-163;		
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Db	37	ATCATGACCTGCTCCCTCTCCTCTCCTCACCCCTTCTCATTTCACTGCACAGGGTCTCTGGCC	96	
Qy	61	GAGTCTGTCTTGACACAGCCGCCCTCAGTGTCTGGGCCCCAGGGCAGAAAGGTCAACATC	120	
Db	97	CAGTCTGTGTGACGACGCCGCCCTCAGTGTCTGGGCCCCAGACACAGAGGGTCACCATC	156	
Qy	121	TCGTGCACTGGAGAGCACTCCAAACATTTGGAGGTTATGATCTACATTTGGTACACAGAGTC	188	
Db	157	TCCTGTCTCTGGAAGCACTCCAAACATTTGGGAATAATTATGTCTCTCTGTACACAGAGTTC	216	
Qy	181	CCAGGAAGCGCCCCAAACTCCTCATCTATGACATTAACAGGCACACCTCAGGAATTTCT	240	
Db	217	CCAGGAACAGCCCCAAACTCCTCATTTATGACAAATTAATAGGCACCCCTCAGGGATTTCT	276	
Qy	241	GACCGATTTCTGTGCTCCAGTCTGGTAC - CGCGGCCCTCCCTGGCCATCACTTGGGCTCCA	299	
Db	277	GACCGATTTCTGTGCTCCAGTCTGGACGTTTCAAGCTTCCCTGGGCATCACCGAGCTCCA	336	
Qy	300	GACTGAGATGAGGCTGATTAATTACTGCCAGTCTCTATGACAGCAGCTGGAATGTCTAGGT	359	
Db	337	GACTGGGGACGAGGCGGATTTATTACTGCGGAACATGGGATAGAAAGACTGAGTGTCTGGGT	396	
Qy	360	ATTCGGAGGAGGACCGGCTGACCGTCTAGGTCAGCCCAAGGCTGCCCCCTCGGTAC	419	
Db	397	GTTTCGGCGAGGGACCAAGCTGACCGTCTTAGTTCAGCCCAAGGCTGCCCCCTCGGTAC	456	
Qy	420	TCTGTTCCCGCCCTCTCTGAGGAGCTTTCAAGCCAAACAAGGCCACACTGGTGTGTCTCAT	479	
Db	457	TCTGTTCCCGCCCTCTCTGAGGAGCTTTCAAGCCAAACAAGGCCACACTGGTGTGTCTCAT	516	
Qy	480	AAGTGACTTTCTACCGGGAGCGGTGACAGTGGCTTGAAGCGCAGATAGCAGCCCGTCAA	539	
Db	517	AAGTGACTTTCTACCGGGAGCGGTGACAGTGGCTTGAAGCGCAGATAGCAGCCCGTCAA	576	
Qy	540	GGCGGGAGTGGAGACCAACACCCCTCCAAACAAGCAACAAGTACGGGGCCAGCAG	599	
Db	577	GGCGGGAGTGGAGACCAACACCCCTCCAAACAAGCAACAAGTACGGGGCCAGCAG	636	
Qy	600	CTACTCTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAAAGCTACAGCTGCCAGGTCAAC	659	
Db	637	CTACTCTGAGCCTGACGCTGAGCAGTGGAGTCCCAAAAAGCTACAGCTGCCAGGTCAAC	696	
Qy	660	GCATGAAGGGAGCACCGTGGAGAGACAGTGGGCCCTTACGAATGTTTCAAT	709	
Db	697	GCATGAAGGGAGCACCGTGGAGAGACAGTGGGCCCTTACGAATGTTTCAAT	746	

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RESULT 7
US-158-646-71
; Sequence 71, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; PRIOR FILING DATE: 2002-05-29
; CURRENT APPLICATION NUMBER: 60/295,239
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 71
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1101637.17
; US-158-646-71

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	Query Match	77.4%; Score 550.6; DB 9; Length 888;	
	Best Local Similarity	86.0%; Pred. No. 1.4e-162;	
	Matches 610; Conservative 0; Mismatches 199; Indels 0; Gaps 0		
Qy	1	ATGAGGGTCCCGCTCAGCTCCTGGGGCTCTGTGCTCTGGCTCCCAGGTGCACGATGT	60
Db	36	ATCATGACCTGCTCGCTCTCTCTCTCAACCTTCATTCACTGACAGGGTCTCTGGGCC	95
Qy	61	GAGTCTGTCTTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGCGACAGAAGTGCACCATC	120
Db	96	CAGTCTGTCTTGACGACAGCCGCCCTCAGTGTCTGGGGCCCCAGGTCAGNAGTGCACCATC	155
Qy	121	TCGTGCACTGGGAGCACCTCAACANTTGGAGTTATGATCTACATTGGTACACAGAGTCT	180
Db	156	TCCTGCTCTGGAAGCAGCTCTAAACATTTGGCTATAATTAATGTTATCTCTGGTACACAGAGTCT	215
Qy	181	CCAGGAAGCGGCCCCAACAATCCTCATCTATGACATTAACAGCGACCCCTCAGGAATTTCT	240
Db	216	CCAGGAGCAGTCCCCCAAAGTCTCTGTATTATGAAAATCAGAAGCGACCCCTCGGGGATTCTCT	275
Qy	241	GACCGATTCTCTGGCTCCAAGTCTGTFAPCCGGGCTCCCTGGGCCATCAGTGGGCTCCAG	300
Db	276	GACCGATTCTCTGGCTCCAAGTCTGGACAGTCAGCCACCCCTGGGGCATCACCGGATCCAG	335
Qy	301	ACTGAGTAGGGCTGATTATTACTGCCAGTCCCTATGACAGCAGCGCTGAATGCTCAGGTA	360
Db	336	ACTGGGACGAGGCCGATTATTACTGCCAATTTGGGATGTCAATCTGAA TGTGGGGTG	395
Qy	361	TTCGAGAGAGGGAACCGGCTGACCGTCTTAGGTTCAGGCCAAGGTCGCCCTTCGGTCACT	420
Db	396	TTCGGCGGAGGGAACCAAGCTGACCGTCTTAAGTCAGCGCAAGGCTGCCCTTCGGTCACT	455
Qy	421	CTGTTCGCGCCCTCTCTTGAGGAGTTTCAAGCCACAGGGCCACACTGGTGTCTCATATA	480
Db	456	CTGTTCGCGCCCTCTCTCTGAGGAGCTTCAAGCCAACAGGGCCACACTGGTGTCTCATATA	515
Qy	481	AGTGACTTTCTACCCGGGAGCCGTGACAGTGGCCCTTGGAAAGGCAGATAGACGCCCTCAAG	540
Db	516	AGTGACTTTCTACCCGGGAGCCGTGACAGTGGCCCTTGGAAAGGCAGATAGCAGCCCTCAAG	575
Qy	541	CGGGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACGCGGCCACGACG	600
Db	576	CGGGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGTACGCGGCCACGACG	635
Qy	601	TACCTGAGCCTGAGCCCTGAGCGTGGAAAGTCCCAACAGAGCTACAGTTCGAGGTCAAG	660
Db	636	TACCTGAGCCTGAGCCCTGAGCGTGGAAAGTCCCAACAGAGCTACAGTTCGAGGTCAAG	695


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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..705
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..705
US-09-948-4298-1

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Query Match	Score	Length
Best Local Similarity	76.0%	540.2; DB 9;
Matches 612; Conservative	86.1%;	Pred. NO. 2.4e-159;
Matches 612; Conservative	0;	Mismatches 93; Indels 6; Gaps 1

Qy	1	ATGAGGTCCCGCTCAGCTCCTCGGGGCTCTCTGCTGCTCTGGCTCCCAAGTGCAAGATGT	60
Db	1	ATGAGGTCCCGCTCAGCTCCTCGGGGCTCTCTGCTGCTCTGGCTCCCAAGTGCAAGATGT	60
Qy	61	GAGTCTGTCGTGACACAGCCGCCCTCAGTGTCTGGGGCCCGAGGCGAGAGGTCAACATC	120
Db	61	GCCTATGAACCTGACTCAGCCACCCTCGGTGTGAGTGTCCCAGGACACAGCGCCAGGATC	120
Qy	121	TCGTGCATCTGGGAGCACCTCCAAACATTGAGAGTTATGATCTACATTGGTACCAGCAGCTC	180
Db	121	ACCTGTGGGG-----AGACAAACAGTAGAATGATATGTCCACTGGTACCGACAGAG	174
Qy	181	CCAGGAACGGCCCCAAACTCCTCATCTATGACATTAACAAGCGACCTTCAGGAATTTCT	240
Db	175	CCAGCGGGGCCCTATACTGTGCATCTATGATGATGTACCGGCCCTCAGGGATCCCT	234
Qy	241	GACCGATTCTTGCTCCAGTCTGGTACCGGGGCTCCCTGGGCCATCACTGGGCTCCAG	300
Db	235	GAGCGATTCTTGCTCCAAATCAGGGAACACCGCCACCTTGACCATCAACGGGGTCGAG	294
Qy	301	ACTGAGGATGAGGTGATTATTACTGCCAGTCTATGACAGCAGCGCTGAATGCTCAGGTA	360
Db	295	GCCGGGATGAGGTGACTATTATGTCAGGTGTGGACAGGGCTAGTGATCATCCGGTC	354
Qy	361	TTCCGAGGAGGGAACCGGCTGACCGTCTTAGGTACGCCAAGGCTGCCCTCGGTCACT	420
Db	355	TTCCGAGGAGGGAACCGGCTGACCGTCTAGGTACGCCAAGGCTGCCCTCGGTCACT	414
Qy	421	CTGTTCCGCGCCTCTCTGAGGAGTTCAAGCAAACAAGGCCACACTGGTGTCTCATATA	480
Db	415	CTGTTCCGCGCCTCTCTGAGGAGTTCAAGCAAACAAGGCCACACTGGTGTCTCATATA	474
Qy	481	AGTGACTTCTACCCGGGACCGTGCAGTGGCCTGGAAAGGACGATAGACGCCCGCTCAAG	540
Db	475	AGTGACTTCTACCCGGGACCGTGCAGTGGCCTGGAAAGGACGATAGACGCCCGCTCAAG	534
Qy	541	GCGGGAGTGGAGACCAACACACCCCTCCAAAACAAGCAACAACAGTACGCGGCCAGCAGC	600
Db	535	GCGGGAGTGGAGACCAACACACCCCTCCAAAACAAGCAACAACGATACGCGGCCAGCAGC	594
Qy	601	TACCTGAGCCTGAGCCCTGAGCAGTGGAAAGTCCCAAGAAGCTACAGCTGCCAGGTCAAG	660
Db	595	TACCTGAGCCTGAGCCCTGAGCAGTGGAAAGTCCCAAGAAGCTACAGCTGCCAGGTCAAG	654
Qy	661	CATGAAGGGAGCAACCGTGGAGAGACAGTGGGCCCTACAGAAATGTTTCATGA	711
Db	655	CATGAAGGGAGCAACCGTGGAGAGACAGTGGGCCCTACAGAAATGTTTCATGA	705

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RESULT 10
US-10-073-138-1
; Sequence 1, Application US/10073138
; Publication NO. US20020187146A1
; GENERAL INFORMATION:
APPLICANT: ANDERSON, Darrell R.
HANNA, Nabil
BRMS, Peter
TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE H
AND B7.2 CO-STIMULATORY ANTIGENS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/073,138
FILING DATE: 13-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/746,361
FILING DATE: 08-NOV-1996
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..705
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-073-138-1
Query Match 76.0%; Score 540.2; DB 9; Length 705;
Best Local Similarity 86.1%; Pred.No.2.4e-159;
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1
Qy 1 ATGAGGGTCCCCGGCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCCGAGGTGCACGATGT 60
Db 1 ATGAGGGTCCCCGGCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCCGAGGTGCACGATGT 60
Qy 61 GAGTCTGTCTGACACAGCGGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGTCACCATC 120
Db 61 GCTATGAACACTGACTCAGCCACCCCTCGGTGTCTGCTGCTCTGGCTCCCGAGGAGCATC 120
Qy 121 TGTGTCACTGGGAGCACCTCCAACTTGGAGGTTATGATCTTACATTGGTACCAGCAGCTC 180
Db 121 ACTGTGGGG-----AGACAAACAGTAGAATGAATATGTCCACTGGTACCAGCAAG 174
Qy 181 CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAAACAGCGACCCCTCAGGAATTTCT 240
Db 175 CCAGCGCGGGCCCTTATCTGTGTCACTATGATGATGACCGGGCCCTCAGGGATCCCT 234

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QY 241 GACCGATTCTCTGGCTCCAAAGTCTGGTACCGCGCCCTCCTGGCCATCACTGGGCTCCAG 300
Db 235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCCACTGACCATCAACGGGTGAG 294
QY 301 ACTGAGATGAGGCTGATTATTAATCTGCGAGTCTCTGACAGCAGCCCTGAATGCTCAGGTA 360
Db 295 GCCGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTC 354
QY 361 TTCGAGGAGGACCGGCTGACCGTCTAGTGCAGCCCAAGGCTGCGCCCTCGGTCACT 420
Db 355 TTCGAGGAGGACCGGCTGACCGTCTAGTGCAGCCCAAGGCTGCGCCCTCGGTCACT 414
QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAAGGCCACACTGGTGTCTCATTA 480
Db 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACAAAGGCCACACTGGTGTCTCATTA 474
QY 481 AGTGACTTACCCGGAGCCGTGACAGTGCCCTGGAAGGAGATGACGCCCGGTCAAG 540
Db 475 AGTGACTTACCCGGAGCCGTGACAGTGCCCTGGAAGGAGATGACGCCCGGTCAAG 534
QY 541 GCGGGAGTGAGACACACACCTCCAAACAAAGCAACAAAGTACCGGCCAGCAGC 600
Db 535 GCGGGAGTGAGACACACACCTCCAAACAAAGCAACAAAGTACCGGCCAGCAGC 594
QY 601 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGGCTACAGCTGCCAGGTCAAG 660
Db 595 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGGCTACAGCTGCCAGGTCAAG 654
QY 661 CATGAAGGAGGACCCGTGAGGAGAGACAGTGCCCTTACAGATGTTTCATGA 711
Db 655 CATGAAGGAGGACCCGTGAGGAGAGACAGTGCCCTTACAGATGTTTCATGA 705

RESULT 11
US-10-001-857-108
; Sequence 108, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Hervé
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Products
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 108
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2005)..(2005)
; OTHER INFORMATION: a, c, g or t
US-10-001-857-108

Query Match 75.2%; Score 534.8; DB 9; Length 2112;
Best Local Similarity 89.4%; Pred. No. 1.5e-157;
Matches 601; Conservative 0; Mismatches 62; Indels 9; Gaps 2;
QY 44 TCCAGGTCCACGATGTGAGTCTGCTCCGACACAGCCGCTCAGTGTCTGGGGCCCCCAG 103
Db 794 TCTAGGTCCTGGGCCAGTCTGTGCTGACGAGCCGCTCAGTGTCTGGGGCCCCCAG 853
QY 104 GCGAGAGGTCAACCTCTGTCGACTGGGAGACCTCCAACTTGAG-----GTTATG 157
Db 854 GCGAGAGGTCAACCTCTCTGCACTGGGAGAGCTCCAACTCGGGGCGAGGTTATGACT 913

QY 158 ATCTACATTGGTGTACGAGCAGCTCCAGGAACGCGCCCAAACTCCTCATCTATGACATTA 217
Db 914 ATGTACACTGGTGTACGAGCAGCTTCAGGNAACAGCCCCCAAACTCATGATTATGAGGTG 973
QY 218 ACAAGCGACCTCTCAGGAATTTCTGACCCGATTTCTTGGTCCAAAGTCTGGTACCGGGCT 277
Db 974 CTAAGCGACCTCTCAGGGGTTTCTGATCGCTTCTTGGTCCAAAGTCTGGCAACAGGGCT 1033
QY 278 CCCTGGCCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCTTATG 337
Db 1034 CCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCTCTCATATG 1093
QY 338 ACAGCAGCCTGAATCTCTCAGGTATTTCGGAGGAGGACCGGCTGACCCGCTCTAGGTCAAG 397
Db 1094 CAGGAGC---TACACTTGGGTGTTCCGGCGGAGGACCAAGCTGACCGCTCTAGGTCAAG 1150
QY 398 CCAAGGCTGCCCCCTCTCGGTCACTCTGTTCCCGCCCTCTCTGAGAGGCTTCAAGCCAA 457
Db 1151 CCAAGGCTGCCCCCTCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAA 1210
QY 458 AGGCCACACTGGTGTGCTCTAAGTGACTTCTACCGGAGCCGCTGACAGTGGCTGGA 517
Db 1211 AGGCCACACTGGTGTGCTCTAAGTGACTTCTACCGGAGCCGCTGACAGTGGCTGGA 1270
QY 518 AGGCAGATAGCAGCCCGCTCAAGGCGGAGTGGAGACCAACACACCTCCAAACAAAGCA 577
Db 1271 AGGCAGATAGCAGCCCGCTCAAGGCGGAGTGGAGACCAACACACCTCCAAACAAAGCA 1330
QY 578 ACAACAAAGTACCGGCCAGCAGTACTGAGCTGACGCTGAGCAGTGGAGTGGAAAGTCCCCA 637
Db 1331 ACAACAAAGTACCGGCCAGCAGTACTGAGCTGACGCTGAGCAGTGGAAAGTCCCCA 1390
QY 638 GAAGCTACAGTCCCGCAGGTCAAGGAGGAGCAGCGTGGAGAGACAGTGGGCCCTTA 697
Db 1391 AAAGCTACAGTCCCGCAGGTCAAGGAGGAGCAGCGTGGAGAGACAGTGGGCCCTTA 1450
QY 698 CAGATGTTTCAT 709
Db 1451 CAGATGTTTCAT 1462

RESULT 12
US-09-954-456-788
; Sequence 788, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 788
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-788

Query Match 74.9%; Score 532.2; DB 10; Length 915;
Best Local Similarity 88.8%; Pred. No. 8.1e-157;
Matches 589; Conservative 0; Mismatches 68; Indels 6; Gaps 1;
QY 47 CAGGTGCAGATGTGAGTCTGCTCTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGC 106
Db 158 CAGGGTCTGGGCCAGTCTGTGCTGACTCAGCCACCTCAGCGTCTGGAGCCCCGGGC 217
QY 107 AGAAGGTACCATCTCTGTCACCTGGGAGCAGCTCCCAACTTGGAGGTATGATCTACATT 166
Db 218 AGAGGTACCATCTCTGTTCTGGAGCGCTCCAACTCTCTATAGTAATATGTTAACT 277
QY 167 GGTACAGAGTCTCCAGGAAAGCGCCCCAACTCTCTATGATGACATTAACAAGCGAC 226
Db 278 GGTACAGAGTCTCCAGGAAAGCGCCCCAACTCTCTATGATGACATTAACAAGCGAC 337
QY 227 CCTCAGGAATTTCTGACCGATTTCTGGCTCCAACTCTCTATGATGACATTAACAAGCGAC 286
Db 338 CCTCAGGGTCTCCAGGAAAGCGCCCCAACTCTCTATGATGACATTAACAAGCGAC 397
QY 287 TCACCTGGGTCCAGACTGAGGATGAGGCTGATTTACTTATGATGACATTAACAAGCGAC 346
Db 398 TCAGTGGGTCTCCAGTCTGAGGATGAGGCTGATTTACTTATGATGACATTAACAAGCGAC 455
QY 347 TGAATGCTCAGGTATTTCCGAGGAGGAGCGCGCTGACCGTCTTAGGTGAGCCCAAGGCTG 406
Db 456 ----TACTGTGTCTTCGCGGAGGAGCAAGCTGACCGTCTTAGGTGAGCCCAAGGCTG 511
QY 407 CCCCCTCGGTCACTCTGTTCCTCGCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 466
Db 512 CCCCCTCGGTCACTCTGTTCCTCGCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 571
QY 467 TGGTGTGTCTATAAGTGACTTCTACCGGAGCGCTGACAGTGGCTGGAAGGCAGATA 526
Db 572 TGGTGTGTCTATAAGTGACTTCTACCGGAGCGCTGACAGTGGCTGGAAGGCAGATA 631
QY 527 GCAGCCCGCTCAAGCGGGAGTGAGACCAACCAACCCCTCCAAACAAAGCAACAAGT 586
Db 632 GCAGCCCGCTCAAGCGGGAGTGAGACCAACCAACCCCTCCAAACAAAGCAACAAGT 691
QY 587 ACAGCGCCAGCAGTACCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACA 646
Db 692 ACAGCGCCAGCAGTACCTGAGCCTGAGCAGTGGAGTCCCAAGAGCTACA 751
QY 647 GCTGCCAGGTACCGATGAAGGAGCAGCGCTGAGAGAGCAGTGGCCCTTACAGATGTT 706
Db 752 GCTGCCAGGTACCGATGAAGGAGCAGCGCTGAGAGAGCAGTGGCCCTTACAGATGTT 811
QY 707 CAT 709
Db 812 CAT 814

RESULT 13
US-09-880-107-3743
; Sequence 3743, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3743
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57809
US-09-880-107-3743

Query Match 74.9%; Score 532.2; DB 10; Length 915;
Best Local Similarity 88.8%; Pred. No. 8.1e-157;
Matches 589; Conservative 0; Mismatches 68; Indels 6; Gaps 1;
QY 47 CAGGTGCAGATGTGAGTCTGCTCTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGC 106
Db 158 CAGGGTCTGGGCCAGTCTGTGCTGACTCAGCCACCTCAGCGTCTGGAGCCCCGGGC 217
QY 107 AGAAGGTACCATCTCTGTCACCTGGGAGCAGCTCCCAACTTGGAGGTATGATCTACATT 166
Db 218 AGAGGTACCATCTCTGTTCTGGAGCGCTCCAACTCTCTATGATGACATTAACAAGCGAC 277
QY 167 GGTACAGAGTCTCCAGGAAAGCGCCCCAACTCTCTATGATGACATTAACAAGCGAC 226
Db 278 GGTACAGAGTCTCCAGGAAAGCGCCCCAACTCTCTATGATGACATTAACAAGCGAC 337
QY 227 CCTCAGGAATTTCTGACCGATTTCTGGCTCCAACTCTCTATGATGACATTAACAAGCGAC 286
Db 338 CCTCAGGGTCTCCAGGAAAGCGCCCCAACTCTCTATGATGACATTAACAAGCGAC 397
QY 287 TCACCTGGGTCCAGACTGAGGATGAGGCTGATTTACTTATGATGACATTAACAAGCGAC 346
Db 398 TCAGTGGGTCTCCAGTCTGAGGATGAGGCTGATTTACTTATGATGACATTAACAAGCGAC 455
QY 347 TGAATGCTCAGGTATTTCCGAGGAGGAGCGCGCTGACCGTCTTAGGTGAGCCCAAGGCTG 406
Db 456 ----TACTGTGTCTTCGCGGAGGAGCAAGCTGACCGTCTTAGGTGAGCCCAAGGCTG 511
QY 407 CCCCCTCGGTCACTCTGTTCCTCGCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 466
Db 512 CCCCCTCGGTCACTCTGTTCCTCGCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 571
QY 467 TGGTGTGTCTATAAGTGACTTCTACCGGAGCGCTGACAGTGGCTGGAAGGCAGATA 526
Db 572 TGGTGTGTCTATAAGTGACTTCTACCGGAGCGCTGACAGTGGCTGGAAGGCAGATA 631
QY 527 GCAGCCCGCTCAAGCGGGAGTGAGACCAACCAACCCCTCCAAACAAAGCAACAAGT 586
Db 632 GCAGCCCGCTCAAGCGGGAGTGAGACCAACCAACCCCTCCAAACAAAGCAACAAGT 691
QY 587 ACAGCGCCAGCAGTACCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACA 646
Db 692 ACAGCGCCAGCAGTACCTGAGCCTGAGCAGTGGAGTCCCAAGAGCTACA 751
QY 647 GCTGCCAGGTACCGATGAAGGAGCAGCGCTGAGAGAGCAGTGGCCCTTACAGATGTT 706
Db 752 GCTGCCAGGTACCGATGAAGGAGCAGCGCTGAGAGAGCAGTGGCCCTTACAGATGTT 811
QY 707 CAT 709
Db 812 CAT 814

RESULT 14
US-10-158-646-73
; Sequence 73, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:

QY 433 TCCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGGTGTGTCTCTATAAGTCACTTCTAC 492
|||
Db 450 TCCTCTGAGGAGCTTCAAGCCAAACAGGCCACACTGGTGTGTCTCTATAAGTCACTTCTAC 509
|||
QY 493 CCGGGAGCCGTGACAGTGGCCTGGGAAGGCAGATAGCAGCCCCGTCAAGCGGGAGTGGAG 552
|||
Db 510 CCGGGAGCCGTGACAGTGGCCTGGGAAGGCAGATAGCAGCCCCGTCAAGCGGGAGTGGAG 569
|||
QY 553 ACCACCACACCCCTCCAAACAAAGCAACAACAAGTACCGCGGCCAGCAGCTTACCTGAGCCTG 612
|||
Db 570 ACCACCACACCCCTCCAAACAAAGCAACAACAAGTACCGCGGCCAGCAGCTTACCTGAGCCTG 629
|||
QY 613 AGCCTGACAGTGGGAAGTCCACAGAACTACAGCTGCAGGTCAAGCATGAAGGAGC 672
|||
Db 630 AGCCTGACAGTGGGAAGTCCACAAAGCTACAGTGCAGGTCAAGCATGAAGGAGC 689
|||
QY 673 ACCGTGGAGAAGACAGTGGCCCTACAGAAATGTTTCA 709
|||
Db 690 ACCGTGGAGAAGACAGTGGCCCTACAGAAATGTTTCA 726
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Search completed: June 3, 2003, 23:03:41
Job time : 95.7363 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:26:38 ; Search time 40.5526 Seconds
(without alignments)
5376.898 Million cell updates/sec

Title: US-09-576-424-9
Perfect score: 711
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/1/ina/5B COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	711	3	US-08-487-550-9
2	582.6	81.9	935	3	US-09-049-672A-20
3	540.2	76.0	705	3	US-08-487-550-1
4	530.2	74.6	895	3	US-09-049-672A-25
5	510.6	71.8	891	3	US-09-049-672A-23
6	502.6	70.7	902	2	US-08-378-939-11
7	484.2	68.1	885	4	US-09-152-060-47
8	482.6	67.9	879	4	US-09-152-060-29
9	468.4	65.9	702	3	US-08-523-894-5
10	416.4	58.6	919	3	US-09-049-672A-24
11	412	57.9	928	4	US-09-152-060-46
12	367.4	51.7	716	4	US-08-793-450-5
13	323.6	45.5	584	4	US-09-404-879A-268
14	306.2	43.1	771	4	US-08-991-789A-241
15	306.2	43.1	771	4	US-09-062-451-241
16	306.4	43.1	771	4	US-09-598-326-241
17	264.4	37.2	408	4	US-09-025-769B-169
18	255.4	35.9	393	1	US-08-305-683A-3
19	254.8	35.8	933	4	US-09-079-029-8
20	253.2	35.6	642	2	US-08-634-783A-4
21	253.2	35.6	642	3	US-09-070-817-4
22	246.8	34.7	346	2	US-08-761-277A-50
23	244.2	34.3	330	4	US-09-240-274-132
24	242.4	34.1	318	2	US-08-646-981-4
25	242.4	34.1	333	2	US-08-477-553A-43
26	242.2	34.1	774	2	US-08-665-202-4
27	242.2	34.1	908	4	US-09-273-839A-9

28	241.2	33.9	327	4	US-09-240-274-223	Sequence 223, App
29	237.6	33.4	333	1	US-08-264-093-5	Sequence 5, Appl
30	236.6	33.3	396	2	US-08-345-321-3	Sequence 3, Appl
31	234.8	33.0	327	4	US-09-240-274-128	Sequence 128, App
32	233.2	32.8	327	4	US-09-240-274-126	Sequence 126, App
33	231.6	32.6	327	4	US-09-240-274-129	Sequence 129, App
34	231.6	32.6	327	4	US-09-240-274-130	Sequence 130, App
35	226.6	31.9	330	1	US-08-199-911-1	Sequence 1, Appl
36	226.6	31.9	336	4	US-09-240-274-133	Sequence 133, App
37	226.4	31.8	318	1	US-08-436-463-9	Sequence 9, Appl
38	226.4	31.8	318	1	US-08-024-253-9	Sequence 9, Appl
39	223	31.4	330	4	US-09-240-274-134	Sequence 134, App
40	220.4	31.0	327	4	US-09-240-274-123	Sequence 123, App
41	220.4	31.0	327	4	US-09-240-274-123	Sequence 123, App
42	217.4	30.6	342	4	US-09-240-274-131	Sequence 131, App
43	216.2	30.4	327	4	US-09-240-274-124	Sequence 124, App
44	208.8	29.4	333	2	US-08-652-816A-27	Sequence 27, Appl
45	204.4	28.7	327	4	US-09-240-274-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-08-487-550-9
; Sequence 9, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMITIVIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; FEATURE:
; MOLECULE TYPE: peptide
; NAME/KEY: CDS
; LOCATION: 1..711
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..711
US-08-487-550-9

Query Match 100.0%; Score 711; DB 3; Length 711;

Db 614 GCGGAGTGGAGACCAACACACCCCTCCAAACAAAGCAACAAAGTACCGGCCAGCAGC 673
Qy 601 TACCTGAGCCTGACCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTTCAG 660
Db 674 TACCTGAGCCTGACCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGGTTCAG 733
Qy 661 CATGAAGGAGCAGCGTGAGAGAGCAGTGGCCCTTACAGATGTTTCAT 709
Db 734 CATGAAGGAGCAGCGTGAGAGAGCAGTGGCCCTTACAGATGTTTCAT 782

RESULT 3

US-08-487-550-1
; Sequence 1, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..705
US-08-487-550-1

Query Match 76.0%; Score 540.2; DB 3; Length 705;
Best Local Similarity 86.1%; Pred. No. 3,7e-140;
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;
Qy 1 ATGAGGGTCCCGCTCAGCTCTGGGGTCTCTGGCTCTGGCTCCCGAGTGCAGATGT 60
Db 1 ATGAGGGTCCCGCTCAGCTCTGGGGTCTCTGGCTCTGGCTCCCGAGTGCAGATGT 60
Qy 61 GAGTCTGTCTGACACAGCCCGCTCAGTGTCTGGGGCCCGCAGGCGCAGAGTCCACATC 120
Db 61 GCCTATGAACCTGACTCAGCCACCTCGGTGTGAGTGTCTGGGGCCCGCAGGAGTCCAGATC 120

Qy 121 TCGTCACTGGGAGCACCTCCACATTGGAGGTTATGATCTATCATTTGGTACAGCAGCTC 180
Db 121 ACCTGTGGGG-----AGACAACAGATGAATATGTCCACTGGTACCAGCAGAG 174
Qy 181 CCAGAAACGGCCCCCAAACTCCTCATCTATGACATTAAACAAGCGACCTCTCAGGAATTTCT 240
Db 175 CCAGCGCGGCCCCCTATCTACTTGTGTCTATGATGATGATGATGATGATGATGATGATGAT 234
Qy 241 GACCAATTCTCTGGCTCCAAAGTCTGGTACCGCGGCTCCTTGGGCGCATCATCTGGGTCCAG 300
Db 235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCTTGACCATCAACGGGGTTCGAG 294
Qy 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCCTGATCTCAGGTA 360
Db 295 GCGGGGATGAGGCTGACTATTACTGTGAGGTGTGGGACAGGGCTAGTGATCATCCGGTC 354
Qy 361 TTGGGAGGAGGACCCCGCTGACCGCTCCTAGGTGAGCCCAAGGCTGCCCTCGGTCACT 420
Db 355 TTGGGAGGAGGACCCCGGTGACCGTCTAGGTGAGCCCAAGGCTGCCCTCGGTCACT 414
Qy 421 CTGTTCCCGCTCCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGTGTCTCATA 480
Db 415 CTGTTCCCGCTCCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGTGTCTCATA 474
Qy 481 AGTGACTTCTACCGGGAGCGGTGACAGTGGCTGGAAGGAGAGTAGAGCCCGTCAAG 540
Db 475 AGTGACTTCTACCGGGAGCGGTGACAGTGGCTGGAAGGAGAGTAGAGCCCGTCAAG 534
Qy 541 GCGGAGTGGAGACCAACACACCCCTCCAAACAAGCAACAAGTACGCGGCCAGCAGC 600
Db 535 GCGGAGTGGAGACCAACACACCCCTCCAAACAAGCAACAAGTACGCGGCCAGCAGC 594
Qy 601 TACCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTCAGC 660
Db 595 TACCTGAGCCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGTGCAGGTCAGC 654
Qy 661 CATGAAGGAGCAGCGTGAGAGAGCAGTGGCCCTTACAGATGTTTCATGA 711
Db 655 CATGAAGGAGCAGCGTGAGAGAGCAGTGGCCCTTACAGATGTTTCATGA 705

RESULT 4

US-09-049-672A-25
; Sequence 25, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guebler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 74.6%; Score 530.2; DB 3; Length 895;
FILING DATE: 71.8%; Score 510.6; DB 3; Length 891;
ATTORNEY/AGENT INFORMATION: Best Local Similarity 84.5%; Pred. No. 6e-132;
NAME: Cerrone, Michael C. Matches 599; Conservative 0; Mismatches 104; Indels 6; Gaps 2;
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0355
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 895 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTUT13
CLONE: 3116314
US-09-049-672A-25

Query Match 74.6%; Score 530.2; DB 3; Length 895;
Best Local Similarity 87.5%; Pred. No. 2.3e-137;
Matches 580; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 47 CAGGTGACAGTGTGAGTCTCTCTGACACAGCGCGCCCTCAGTGTCTGGGGCCCGCAGGCG 106
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QY 107 AGAAGTCAACATCTGTGTCATCTGGAGCACCTTCAACATTTGGAGTTATGATCTACATT 166
DB 140 AGAGGGTCAACATCTCTTCTTGGAAACCACTTCAACATCTCAAGTAACTTCTGTGCAAT 199
QY 167 GTTACACAGCAGTCCCGAGGAGCGGCCCAAACTCTCATCTATGACATTACAGCGAC 226
DB 200 GTTACCAATTAGTTCAGAGGAGCGGCCCAAACTCTCATCTATGATGATGACGGTG 259
QY 227 CTTCAAGGATTTCTGACCGATTTCTTGGTCTCAAGTCTGGTACCGGGCTCCCTGGGCA 286
DB 260 CTTCCGGGTCTCTGACCGATTTCTTGGTCTCAAGTCTGGACCTCAGCTCCCTGGCA 319
QY 287 TCATGGGCTCAGACTGAGGATGAGGCTGATTTATCTGCGCAGTCTCTATGACAGGCG 346
DB 320 TCAGTGGGCTCCGGCCGAGGATGAACTGATTTACTGTGCAACATGGGATGACAGTG 379
QY 347 TGAATGCTCAGGTATTCGAGGAGGAGCCCGGCTGACCGTCTAGTGTGACCGCCAGGCTG 406
DB 380 TCAGTGGTGGATGTTCCGGCGGAGGACCAAGCTGACCGTCTTAGTGTGACCGCCAGGCTG 439
QY 407 CCCCCCTCGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCACAC 466
DB 440 CCCCCCTCGTCACTCTGTTCCCACTCTCTGAGGAGCTTCAAGCCAAAGGCCACAC 499
QY 467 TGGTGTCTCATAAGTACTTCTTACCGGGAGCGCTGACAGTGGCTGGAAGGAGATA 526
DB 500 TGGTGTCTCATAAGTACTTCTTACCGGGAGCGCTGACAGTGGCTGGAAGGAGATA 559
QY 527 GCAGCCCGCTCAAGCGGGAGTGGAGACCAACACACCTTCCAAACAAAGCCACAAAGT 586
DB 560 GCAGCCCGCTCAAGCGGGAGTGGAGACCAACACACCTTCCAAACAAAGCCACAAAGT 619
QY 587 AGCGGGCCAGCAGTCACTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAGCTACA 646
DB 620 AGCGGGCCAGCAGTCACTGAGCCTGAGCAGTGGAGTCCCAAGAGCTACA 679
QY 647 GTCGCAAGTCAAGTAAAGGAGCAGCTGGAGAGACAGTGGCCCTTACAGATGTT 706
DB 680 GTCGCAAGTCAAGTAAAGGAGCAGCTGGAGAGACAGTGGCCCTTACAGATGTT 739
QY 707 CAT 709
DB 740 CAT 742

RESULT 5

US-09-049-672A-23
Sequence 23, Application US/09049672A
Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049,672A

FILING DATE: HERewith

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0497 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 891 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: THYNOT10

CLONE: 2872705

US-09-049-672A-23

Query Match

Best Local Similarity 84.5%; Pred. No. 6e-132;

Matches 599; Conservative 0; Mismatches 104; Indels 6; Gaps 2;

QY 4 AGGTGCCGCTCAGCTCCTGGGGCTCTGTGCTCTGGTCCCGAGGTGACGATGTGAG 63
DB 34 ATGGCTGGGCTCTGCTATTCTCACCCTCTCACTCAGGGGCACAGGGTCTCTGGGCCAG 93
QY 64 TCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGGCAGCAAGGTCAACATCTCG 123
DB 94 TCTGCCCTGATCAGCCTGCTCGGTGTCTGGGTCTCTGGACATCGATCAACATCTCC 153
QY 124 TGCACCTGGAGCACCTCCCAACATTGGAGGTTAT---GATCTACATTGGTACAGCAGCTC 180
DB 154 TGCACCTGGAACACAGCAGTGTGCTGTTGTTATTAATACTATGCTCTCTGGTACCAAGTCC 213
QY 181 CCAGAACGGCCCGCAAACTCTCATCATGACATTAAACAGCGACCTCAGGAATTTCT 240
DB 214 CCAGCACGGCCCGCAAACTCATGATTTATGAGGTGAGTAAATCGGCCCTCAGGGGTTTCT 273


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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-152-060-47

Query Match      58.1%; Score 484.2; DB 4; Length 885;
Best Local Similarity 80.9%; Pred. No. 1.2e-124;
Matches 564; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 13 GCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCAGGTGACGATGTGAGTCTGTCCTG 72
Db 30 GTTCTGCTCTCTGACCTCTCTCACTCACTGTGAGTGTGAGTGTGAGGAGGCTG 89
QY 73 ACACAGCGCGCTCAGTGTCTGGGGCCCGAGGACAGAGTTCACCATCTCTGTCAGTGG 132
Db 90 ACTCAGCGCCCTCGGTGTCTGAAGGACTTGACAGACAGCCGACACTCACCTGCACCGG 149
QY 133 AGCACTTCCAACTTGGAGGTATGATCTACATTTGATGACAGAGTCTCCAGGACGGCC 192
Db 150 AACAAACAATGTTGGGACCAAGGAGGAGCTTGGCTGCAGCAGCAGGCGCCACCT 209
QY 193 CCCAAACTCTCATCTATGACATTAAAGCGACCTCTCAGGAAATTTCTGACCGATTCTCT 252
Db 210 CCCAAACTCTGCTCTACAGGATATATAACCGGCCCTCAGGATCTCAGAGATTATCT 269
QY 253 GGTCTCAAGTGTGGTACCGCGCTCTCCCTGGCCATCATCTGGCTCCAGATCAGGATGAG 312
Db 270 GCATTCAGGTTCAGGAGCCACATCTCTCCCTGACCATTTACTGGACTCCAGCTCAGGACGAG 329
QY 313 GCTGATTATTTACTGTCAGTCTTATGACAGCAGCCTGAATGCTCAGTATTTCCAGGAGGG 372
Db 330 GCTGATTATTTACTGTCGACGATATGACAGCAGCCTCGCAGTTGGAGTTTCCGCGAGGG 389
QY 373 ACCCGCTCAGCGCTCTAGGTGAGCCCAAGGCTGCGCCCTCGGTCTCACTCTGTTCCCGCCC 432
Db 390 ACCAAGTACCGCTCTTAGTTCAGCCCAAGGCTGCGCCCTCGGTCTCACTCTGTTCCACCC 449
QY 433 TCCTCTGAGGAGTTCAAGCCCAAGGCGCACACTGGTGTGTCTATAGTCACTTCTTAC 492
Db 450 TCCTCTGAGGAGTTCAAGCCCAAGGCGCACACTGGTGTGTCTATAGTCACTTCTTAC 509
QY 493 CCGGGAGCGGTGACAGTGTGCTGGAGGAGGAGTAGAGCCCGCTCAAGCGGGAGTGGAG 552
Db 510 CCGGGAGCGGTGACAGTGTGCTGGAGGAGGAGTAGAGCCCGCTCAAGCGGGAGTGGAG 569

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-152-060-29

Query Match      67.9%; Score 482.6; DB 4; Length 879;
Best Local Similarity 80.8%; Pred. No. 3.2e-124;
Matches 563; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 13 GCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCAGGTGACGATGTGAGTCTGTCCTG 72
Db 22 GTTCTGCTCTCTCTGACCTCTCTCACTCACTGTGAGTGTGAGTGTGAGGAGGCTG 81
QY 73 ACACAGCGCGCTCAGTGTCTGGGGCCCGAGGACAGAGGTTCACCATCTCTGTCAGTGG 132
Db 82 ACTCAGCGCCCTCGGTGTCTCAAGGACTTGACAGACAGCCGACACTCACCTGCACCGGG 141
QY 133 AGCACTTCCAACTTGGAGGTATGATCTACATTTGATGACAGAGTCTCCAGGACGGCC 192
Db 142 AACAAACAATGTTGGGACCAAGGAGGAGCTTGGCTGTCAGCAGCAGCAGGCGCCACCT 201
QY 193 CCCAAACTCTCATCTATGACATTAAAGCGACCGCTCAGGAAATTTCTGACCGATTCTCT 252
Db 202 CCCAAACTCTCTGCTCTCAGGATATATAACCGGCCCTCAGGATCTCAGAGATTATCT 261
QY 253 GGTCTCAAGTGTGGTACCGCGCCCTCTCTGCGCCATCTCTGCGCTCCAGATGAGATGAG 312
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Db 262 GATCCAGTCCAGGACCCACATCTCTCCCTGACCACTTACTGAGCTCCAGCTCAGGACGAG 321
QY 313 GGTGATTATTACTGCGAGTCTTATGATGACGAGCCTGAATGCTCAGGTATTTCGAGGAGG 372
Db 322 GGTGACTATTACTGCGCAGCATATGACGAGCCTCGCAGTTTGGATGTTTCGCGGAGG 381
QY 373 ACCCGCTACCGTCTAGTTCAGTCCCAAGGCTGCCCCCTCGTCACTCTGTTCGCGCC 432
Db 382 ACCAAGCTACCGTCTAGTTCAGTCCCAAGGCTGCCCCCTCGTCACTCTGTTCGCGCC 441
QY 433 TCTCTGAGGAGCTTCAAGCACAAGGCGCACACTGTGTCTCATAAGTACTTCTAC 492
Db 442 TCTCTGAGGAGCTTCAAGCACAAGGCGCACACTGTGTCTCATAAGTACTTCTAC 501
QY 493 CCGGGAGCGGTGACAGTCCGTTGAAGGAGATAGCAGCCCCCGTCAAGCGGAGTGGAG 552
Db 502 CCGGGAGCGGTGACAGTCCGTTGAAGGAGATAGCAGCCCCCGTCAAGCGGAGTGGAG 561
QY 553 ACCACACACCTTCCAAACAGAGCAACAAGGAGTACGCGGCCAGGAGTACCTGAGCCTG 612
Db 562 ACCACACACCTTCCAAACAGAGCAACAAGGAGTACGCGGCCAGGAGTACCTGAGCCTG 621
QY 613 AGCCTGAGCAGTGGAGTCCCAAGGAGTACGCGGCCAGGAGTACCTGAGCCTG 672
Db 622 AGCCTGAGCAGTGGAGTCCCAAGGAGTACGCGGCCAGGAGTACCTGAGCCTG 681
QY 673 ACCGTGAGGAGACAGTGGCGCCCTACAGAAATGTTTCAT 709
Db 682 ACCGTGAGGAGACAGTGGCGCCCTACAGAAATGTTTCAT 718

RESULT 9

US-08-523-894-5
; Sequence 5, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Refi, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: lambda variable and constant domains in
; CHROMOSOME/SEGMENT: CE9.1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..702
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..702
; US-08-523-894-5

Query Match 65.9%; Score 468.4; DB 3; Length 702;

Best Local Similarity 79.9%; Pred. No. 2.5e-120;

Matches 566; Conservative 0; Mismatches 136; Indels 6; Gaps 1;

QY 4 AGGGTCCCCCGCTCAGCTCCTGGGGCTCTGCTGCTCTGGCTCCAGGTGACGATGTGAG 63

Db 1 ATGGCTGGGCTCTGCTGCTCTCGGCTCTTGTCTACTTTACAGACTCTGGGGCTCC 60

QY 64 TCTGTCTTGACACAGCGGCCCTCAGTGTCTGGGGCCCCCAGGCGAGAAAGTTCACATCTCG 123

Db 61 TATGAGTTGAGTCAGCTCGCTCAGTGTCCGTGTCCTCCAGGACAGAGG-----CGGG 114

QY 124 TGCATGGGAGCACCTCCAACTTGGAGGTTATGATCTACATTTGTTACAGAGCTCCCA 183

Db 115 TTTCACTGTGGGGGAGACAACTTGGAGGAAAGTGTACAGTGTATCCAGCAGAGGCCA 174

QY 184 GGAAGCGGCCCAAACTCTCATCTATGACATTAACAGCGACCTCAGGAATTTCTGAC 243

Db 175 CCGCAGGCCCCCTGTGCTGCTCATCTATGCTGACGAGCAACGGCCCTCAGGGATCCCTGG 234

QY 244 CGATTCTCTGGCTCCAAAGTCTGTGTACCGGGCTCTCCTGGCCATCACTGGGCTCCAGACT 303

Db 235 CGATTCTCTGGCTCCAACTCAGGGAACACCGCCACCTGACCATCAGCGGGGTGAGGCC 294

QY 304 GAGGATGAGGCTGATTTATTTACTTGCAGTCTCTATGACAGCAGCTGTAATGCTCAGGTATT 363

Db 295 GGGGATGAGGCTGACTATTACTTGTGAGGTGTGGGACAGTACTGCTGATCATTTGGGTCTTC 354

QY 364 GGAGGAGGACCGGCTGACCGTCTAGTTCAGCCCAAGGCTGCCCCCTCGTCACTCTG 423

Db 355 GCGGAGGAGACCGGCTGACCGTCTAGTTCAGCCCAAGGCTGCCCCCTCGTCACTCTG 414

QY 424 TTTCCGCGCTCTCTGAGGAGCTTCAAGCACAAGGCGCACACTGTGTCTCTATAAGT 483

Db 415 TTTCCGCGCTCTCTGAGGAGCTTCAAGCACAAGGCGCACACTGTGTCTCTATAAGT 474

QY 484 GACTTCTACCGGGAGCGGTGACAGTGGCTCTGGAAGGCAGATAGCAGCCCGTCAAGGCG 543

Db 475 GACTTCTACCGGGAGCGGTGACAGTGGCTCTGGAAGGCAGATAGCAGCCCGTCAAGGCG 534

QY 544 GGAGTGGAGACACACACACCTCCAAAACAAAGCAACAAGTACGCGGCCAGCAGCTAC 603

Db 535 GGAGTGGAGACACACACACCTCCAAAACAAAGCAACAAGTACGCGGCCAGCAGCTAC 594

QY 604 CTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCCAGGTTCAGCAT 663

Db 595 CTGAGCTGACCGCTGAGCAGTGGAGTCCCAAGAGCTACAGCTGCCAGGTTCAGCAT 654

QY 664 GAAGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCATGA 711

Db 655 GAAGGAGCACCGTGGAGAGACAGTGGCCCTTACAGAAATGTTTCATGA 702

RESULT 10

US-09-049-672A-24
; Sequence 24, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti

APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREMITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Carrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 919 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LMODNOT08
CLONE: 3056213
US-09-049-672A-24

Query Match 58.6%; Score 416.4; DB 3; Length 919;
Best Local Similarity 78.7%; Pred. No. 6.3e-106;
Matches 524; Conservative 0; Mismatches 136; Indels 6; Gaps 2;

QY 47 CAGGTGCAGATGTGAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCAAGGCG 106
DB 106 CAGGATGGATCTCAGACTGTGGTGACCGAGGAGCCATGCTTCAGTGTCCCTGGAG 165
QY 107 AGAGGTACACATCTCGTGACCTGGAGCAC---CTCCAAATTTGAGGTTATGATCTAC 163
DB 166 GGACAGTCACTACTTGTGGCTTGTGAGCTCTGGCTCAGTCTCTACTAGTAACCTACCCCA 225
QY 164 ATTGGTACCAGAGTCCCGAGGACCGCCCAACTCTCATCTATGACATTAACAAGC 223
DB 226 GCTGGTACCAGAGACCCCGAGGCTCCAGCGACGCTCATATACGGCAAGGTGTTTC 285
QY 224 GACCCCTCAGGAATTTCTGACCGATTCTCTGGGTCCAAAGTCTGACCGGCTCCCTGG 283
DB 286 GTTCTTCTGGAGTCCCTGATCGTCTCTGGTCCATCTCTGGACAAAGCGGCTCA 345
QY 284 CCATCACTGGGTCCAGACTGAGGATGAGGCTGATTTACTGCCAGTCTATGACAGCA 343
DB 346 CCATCAGCGGGGCCAGGAGATGATGATCTGATTTATTGTCCTATAT---AGGC 402
QY 344 GCCTGATGCTCAGGTATTTCGGAGGAGGACCGGCTGACCGTCTAGTTCAGCCCAAGG 403
DB 403 GTAGTGGCTCTTGGGGTTCGGCGGAGGAGCAAGCTGTCCTAGTTCAGCCCAAGG 462

QY 404 CTGCCCCCTCGGTCACTCTGTTCGGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCA 463
DB 463 CTGCCCCCTCGGTCACTCTGTTCGGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCA 522
QY 464 CACTGGTGTCTCATAAGTGAAGTCTTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAG 523
DB 523 CACTGGTGTCTCATAAGTGAAGTCTTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAG 582
QY 524 ATAGCAGCCCCGTCAAGGGGGAGTGGAGACCAACACACCCCTCCAAACAAAGCAACA 583
DB 583 ATAGCAGCCCCGTCAAGGGGGAGTGGAGACCAACACACCCCTCCAAACAAAGCAACA 642
QY 584 AGTACGCGGCCAGCAGTACTCTGAGCCCTGAGCAGTGGAGTGGAGTCCCAAGAGCT 643
DB 643 AGTACGCGGCCAGCAGTACTCTGAGCCCTGAGCAGTGGAGTGGAGTCCCAAGAGCT 702
QY 644 ACAGCTGCCAGGTACCGCATGAAGGGAGGACCGTGGAGAAAGACAGTGGCCCTTACAGAA 703
DB 703 ACAGCTGCCAGGTACCGCATGAAGGGAGGACCGTGGAGAAAGACAGTGGCCCTTACAGAA 762
QY 704 GTTCAT 709
DB 763 GTTCAT 768

RESULT 11
US-09-152-060-46/c
Sequence 46, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P1 US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/050,934
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 46
LENGTH: 928
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (49)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (78)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (148)

OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (163)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (532)
OTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-46

Query Match 57.9%; Score 412; DB 4; Length 928;

Best Local Similarity 83.9%; Pred. No. 1e-104;
Matches 464; Conservative 18; Mismatches 69; Indels 2; Gaps 2;

QY 158 ATCTACATTGGTACACAGCTCCAGGACGGCCCC-CAAACTCCTCATCTATGACATT 216
DB 893 ATGTATTATTGGTACCAACAGAGTCAAGCGAGCCCTGTGCTGTCTATGAGGAC 834
QY 217 ACAAGCGACCTCAGGATTTCTGACCGATTCTCTGGCTCCAGTCTGGTACCGGGCC 276
DB 833 AACAAACGACCTCCGG-ATCCCTSAGAGATTCTTGGCTCCAGYTCAGGGACAGTGGCC 775
QY 277 TCCTGGCCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCAT 336
DB 774 ACTTGACTATCAGTGGGCCAGGTGGAGATGCGGCTGACTACTCTGTACTCAACA 715
QY 337 GACAGCAGCTGAATGCTCAGGTATTTCGGAGGAGGACCGGCTGACCGTCTTAGGTCTAG 396
DB 714 GACAGCAGTGGTAATCATGKGCTTCGGAACCTGGGACCAAGGTCACTCTTAGGTCTAG 655
QY 397 CCAAGGTCGCCCTTCGGTCTACTCTGTTCGGCCCTCTCTCTGAGGAGCTTCAAGCAAC 456
DB 654 CCAAGGTCYRMCCCKGCTACTCTGTTCGGCCCTCTCTCTGAGGAGCTYCAAGCAAC 595
QY 457 RAGGCACACTGGTGTCTCATAGTACTTCTACCGGAGCGGTGACAGTGGCCTGG 516
DB 594 RAGGCACACTGGTGTCTCATAGTACTTCTACCGGAGCGGTGACAGTGGCCTGG 535
QY 517 RAGGCAGATGACGAGCCCTCAAGGCGGAGTGGAGACCAACACACCTCCAAACAAAGC 576
DB 534 RAGGCAGATGACGAGCCCTCAAGGCGGAGTGGAGACCAACACCTCCAAACAAAGC 475
QY 577 AACAAAGTACGCGGCCAGCTACTGAGCTGACCTGACCTGAGCAGTGGAGTGGAGTCCAC 636
DB 474 AACAAAGTACGCGGCCAGCTACTGAGCTGACCTGAGCAGTGGAGTGGAGTGGAGTCCAC 415
QY 637 AGAGCTACAGTCCAGCTCAGCTCAGGATGAGGAGCACTGAGGAGAGAGTGGCCTG 696
DB 414 AGAGCTACAGTCCAGCTCAGCTCAGGATGAGGAGCACTGAGGAGAGAGTGGCCTG 355
QY 697 ACAGATGTTTCAT 709
DB 354 ACAGATGTTTCAT 342

RESULT 12

US-08-793-450-5
Sequence 5, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHABATHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON

STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793.450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLCULE TYPE: other nucleic acid
FEATURE:
NAME/KEY: CDS
LOCATION: 1..716
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..57
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..716
OTHER INFORMATION: /product= "IMMUNOGLOBIN, LIGHT"
OTHER INFORMATION: CHAIN"

US-08-793-450-5

Query Match 51.7%; Score 367.4; DB 4; Length 716;

Best Local Similarity 75.2%; Pred. No. 2e-92;
Matches 521; Conservative 0; Mismatches 121; Indels 51; Gaps 3;

QY 47 CAGGTGCAGATGTGAGTCTGCTTGACACACCGCCCTCAGTGTCTGGGGCCCGCAGGCG 106
DB 44 CAGGTGTCACTCCGACATCGAGCTCACTCAGGACCTGCTGTGTCTGTGGCTTTGGGAC 103
QY 107 AGAAGTCCACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 166
DB 104 AGACAGTCAGGATCACATGCCAAGGAGACAGCCTCA-----GAACCTATTATGCAAGCT 157
QY 167 GGTACACAGAGCTCCAGGAAAGCGGCGCCCAAACTCCTCATCTATGACATTAAACAGCGAC 226
DB 158 GGTACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 217
QY 227 CCTCAGGATTTCTGACCGATTCTCTGGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 286
DB 218 CCTCAGGATTTCTGACCGATTCTCTGGCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 277
QY 287 TCACCTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTTGCAGTCTCTATGACAGCAGCC 346
DB 278 TCACCTGGGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 331
QY 347 TGAATGCTCAGGTATTTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 406
DB 332 -----AGGTGTTTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 382
QY 407 CCCCCCTCGTCACTCTGTTCGGCCCTCC-----T 436
DB 383 CCCCCCTCGTCACTCTGTTCGGCCCTCCCTCGAGGAGCTTCAAGCCAAACAGGCGCACAC 442

QY 437 CTGAGGAGCTTCAAGCAACCAAGGCCACACTGGTGTCTCATAGTACTTCTACCCGG 496
DB 443 TCAGGAGCTTCAAGCAACCAAGGCCACACTAGTGTGTCTCATAGTACTTCTACCCGG 502
QY 497 GAGCCCTGACAGTGGCTTGAAGGAGATAGCAGCCCGTCAAGGCGGAGTGGAGCCA 556
DB 503 GAGCTGTGACATTTGGCTTGAAGGAGATAGCAGCCCGTCAAGGCGGAGTGGAGCCA 562
QY 557 CCACACCTCCAAACAAAGCAACCAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGC 616
DB 563 ACAACCTCCAAACAGAGCAACCAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGC 622
QY 617 CTGAGCAGTGGAGTCCACAGAGCTACAGCTGCGCAGCTACGATGAGGAGCAGCG 676
DB 623 CCGAGCAGTGGAGTCCACAGAGCTACAGCTGCGCAGCTACGATGAGGAGCAGCTG 682
QY 677 TGGAGAGCAGTGGCCCTCAGAGATGTTTAT 709
DB 683 CAGAGAAGCGGTGGCCCTCGAGAATGTTTAT 715

RESULT 13

US-09-404-879A-268/c

; Sequence 268, Application US/09404879A

; Patent No. 6468546

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.462C2

; CURRENT APPLICATION NUMBER: US/09/404,879A

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 393

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 268

; LENGTH: 584

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(584)

; OTHER INFORMATION: n = A,T,C or G

US-09-404-879A-268

Query Match 45.5%; Score 323.6; DB 4; Length 584;
Best Local Similarity 87.3%; Pred. No. 2.3e-80;
Matches 378; Conservative 0; Mismatches 47; Indels 8; Gaps 2;

QY 220 AAGCGACCTCAGGAATTTCTGACCGATTTCTGCGCTCCAGTCTGGTAC-----CGCGG 274
DB 450 AAGCGCCCTCAGGGTCCCTGATCGTTTCTGGCTTCAAGTCTTGGCAACAGGGC 391
QY 275 CTCTCCTGCCATCATCTGGGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 334
DB 390 CTCTCCTTGACGCTCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTTACTCAGCTCAT 331
QY 335 ATGACAGAGCTGATGCTCAGTATTCGGAGGAGGACCGGCTGACCGTCTTAGGTTC 394
DB 330 ATGACAGGCAAC---AACAAATGGGTTCTCGCGGAGGACCAAGCTGACCGTCTTAGGTTC 274
QY 395 AGCCCAAGGCTGCCCTCGGTCACCTCTGTTCCCGGCTCTCTGAGGAGCTTCAAGCA 454
DB 273 AGCCCAAGGCTGCCCTCGGTCACCTCTGTTCCCGGCTCTCTGAGGAGCTTCAAGCA 214
QY 455 ACAAGGCAACACTGGTGTCTCATAAGTGAATTTACCCGGAGCCGTCAGTGGCT 514
DB 213 ACAAGGCAACACTGGTGTCTCATAAGTGAATTTACCCGGAGCCGTCAGTGGCT 154
QY 515 GGAAGGAGATAGCAGCCCGTCAAGGCGGAGTGGAGCACCACACCTCCCAACAA 574

DB 153 GGAAGGAGATAGCAGCCCGTCAAGGCGGAGTGGAGCACCACACCTCCCAACAA 94
QY 575 GCAACAAAGTACGCGCCAGCAGCTACCTGAGCTCAGCCTGAGCAGTGGAAAGTCCC 634
DB 93 GCAACAAAGTACGCGCCAGCAGCTACCTGAGCCTGAGCAGTGGAAAGTCCC 34
QY 635 ACAGAGCTACAG 647
DB 33 ACAGAGCTACAG 21

RESULT 14

US-08-991-789A-241/c

; Sequence 241, Application US/08991789A

; Patent No. 6225054

; GENERAL INFORMATION:

; APPLICANT: Fridakis, Tony N.

; Smith, John M.

; Reed, Steven G.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER

; NUMBER OF SEQUENCES: 292

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed IP Law Group

; STREET: 701 Fifth Avenue, Suite 6300

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/991,789A

; FILING DATE: 11-Dec-1997

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Potter, Jane E. R.

; REGISTRATION NUMBER: 33,332

; REFERENCE/DOCKET NUMBER: 210121.419C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 241:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 771 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; SEQUENCE DESCRIPTION: SEQ ID NO: 241:

US-08-991-789A-241

Query Match 43.1%; Score 306.2; DB 4; Length 771;
Best Local Similarity 83.7%; Pred. No. 1.6e-75;
Matches 370; Conservative 0; Mismatches 66; Indels 6; Gaps 2;

QY 122 CGTCACTGGAGCAGCTCCCAACTTGGAGGTTA---TGATCTACATTGGTACCAGCAGC 178
DB 448 CTGCANTGGAACAGCAGTACGCTTGGTGTATATAATGTCNTGGTACCAGCAGC 389
QY 179 TCCAGGAGCGGCCCCCAACTCTCATCTATGACATTAAAGGACCCCTCAGGAATTT 238
DB 388 ACCGAGCAAGCCCCCAATTCATGATTTATGAGTGGTAATCGGCCCTCAGGGGTTT 329
QY 239 CTGACCGATTCTCTGGCTCCAAAGTCTGGTACCGGGCTCCCTGGCCATCACTGGGCTCC 298
DB 328 CTATCGCTTCTCTGGCTCCAAAGTNTGGCAACAGGCTCCCTGACCATCTCTGGGCTCC 269

[illegible]

RESULT 15

US-09-062-451-241/c
; Sequence 241, Application US/09062451
; Patent No. 6344550

; PACIFIC NO: 0341350
: GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.

APPLICANT: FLUGAKIS, IOLLY
APPLICANT: Smith, John M.

APPLICANT: SMITH, JOHN M.
APPLICANT: Reed, Steven G.

;
; AFFILIANT: REED, STEVEN G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

;	TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR THE
;	TITLE OF INVENTION:	TREATMENT AND DIAGNOSIS OF BREAST CANCER
;		

; TITLE OF INVENTION: IREA
; NUMBER OF SEQUENCES: 297

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESS: SEED and BERRY LLP

ADDRESSEE: SEED and BEAN LIF
STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

```

; COMPILE WITH: 8086
;
; MEDIUM TYPE: Floppy disk
;

```

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

[illegible]

APPLICATION NUMBER: US/09/062,451

FILING DATE: 04-APR-1997

FILED DATE: 0
CLASSIFICATION:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.419C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6

; INFORMATION FOR SEQ ID NO: 241:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 771 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

ORGANISM: *Homo sapiens*

US-09-062-451-241

Query Match	43.1%	Score 306.2;	DB 4;	Length 771;
Best Local Similarity	83.7%	Pred. No. 1.6e-75;		
Matches 370; Conservative	0;	Mismatches 66;	Indels 6;	Gaps 2;

Qy	122	CGTGCACTGGAGCACTCCAACTTGGAGGTTA --- TGATCTACATTTGGTACCAAGCAGC	178
Db	448	CCTGCANTGGAACCAAGCAGCAGTGGTGGTTATAATAATGCTCTCNTGTGATCCAAACAGC	389

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